

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 117161

TO: Nancy Vogel

Location: rem/2a65/2c70

Art Unit: 1636

Monday, March 29, 2004

Case Serial Number: 09/963285

From: Paul Schulwitz

Location: Biotech-Chem Library

REM-1A65

Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Vogel,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (571)272-2527



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PAT 10-APR-2003
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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           /organism='Unidentified'.
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1 (bases 1 to 28)
Cochran,M.D. and Unnker,D.E.
Recombinant swinepox virus
Patent: US 6497882-A 265 24-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                28 bp DN Sequence 265 from patent US 6497882. AR267926 AR267926.1 GI:29698051
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/db_xref="taxon:9606"
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/organism="Homo sapiens"

    .28
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

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/mol_type="genomic DNA"
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BARBARA J WINSLOW, WARK D COCHRAN
C12N15/09, A6IK39/12, A6IK39/125, A6IK39/15, A6IK39/215, A6IK39/23,
A6IK39/245,
A6IK48/00, A6IP43/00, C12N1/00//C07K14/705, C12N15/00 CC FIV
A0WIST FROM Primer
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Recombinant virus expressing foreign DNA encoding feline CD80, Feline CD86, feline CTLA-4 or feline interferon-gamma and uses Patent: JP 200251381-A 75 14-MAY-2002;
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Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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1 (FGBGG I - 0 28)
CCOHTAN, M.D. and Junker, D.E.
FECCOMDINANT SWINGS VITUS
PATENT: US 6221361-A 84 24-APR-2001;
Location/Qualifiers
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Sequence 84 from patent US 6221361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
/mol_type="unassigned DNA"
                                  /organism="unknown"
/mol_type="unassigned DNA"
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17 2002513581-A/75
14-MAY-2002
30-ARE-1999 UP 2000547248
01-MAY-1996 US 09/07171
Location/Qualifiers
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BD273541.1 GI:33083309
JP 2002513581-A/75.
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AR147023.1 GI:15110826
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BD273541/c
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STS 10-JUN-2003

RESULT 6 AF227460/c

ò 셤 DEFINITION ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

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BX322143 19-JUN-2002
Arabidopsis thaliana transposon insertion STS SM_3.35925, sequence
tagged site.
                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MT a mis-expression mutator transposon.

3 denotes a sequence derived from the 3'end of the transposon BBSRC GARNet, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
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/clone="AC006841"
/note="Derived from superpool 25.06 NASC code N41149"
                                                                                                                                                                                                                                                                                                                                                                                                                             Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
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SHGC-100532 Human Homo sapiens STS genomic, sequence sage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/variety="Columbia-0 NASC stock code N1092"
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Mammalia, Butheria, Primates, Catarrhini
1 (baes 1 to 206)
Olivier, M. and Cox, D.R.
Umpublished, Olivier, M., Cox, D.R. (2000)
Unpublished (2000)
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Clarke, J.H.
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Best Local Similarity 100.
Matches 12; Conservative
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1 GGAAAGTAAAA
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Unpublished
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                                                                                                                                                             PLN 13-JUN-2000
                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnollophyta, Liliopsida, Poales, Poaceae, Spermatophyta, Bromeae, Bromeae, Eromus.

(Dases, 1 to 150)

Paulsen, A., Meyer, S.B., Coleman, C.E. and Pairbanks, D.J.

Microsatellite markers for Bromus tectorum (cheatgrass)
Unpublished

(Dases 1 to 150)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Patent: WO 0188188-A 468 22-NOV-2001;
School Juridical Person Nihon University (JP)
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Submitted (21-Jan) Botany and Range Science, Brigh University, 401 WIDB, Provo, UT 84602, USA
Location/Qualifiers
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100.0%; Score 12; DB 6; Length 151;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

	Description	apida	Mus	ນສາ	Ø t	BY664728 Danio rer	AX655393 Sequence	AC124247 Homo sapi	ACUZ/483 ROMO SAPI AL685189 Penicilli	AJ535061 Oryza sat	AC066610 Homo sapi	AC138109 Mus muscu AC021596 Homo sapi	AC146089 Pan trogl	AC079431 Mus muscu	AL684840 Penicilli	BX276102 Danio rer	AC084804 Mus muscu	AC067888 Homo sapi	AC105113 Homo sapi	AC078884 Mus muscu	шо	AC021929 Homo sapi RX469901 Danio rer	82	AC019251 Homo sapi	200	AC023212 Homo sapi	ani			lus lus	ກພ ຮກ		lomo sapi	ğ.	s 0mo!		Sea of Face	661-1414-4T	ene	.; Vertebrata; Euteleostomi;	, committee (1)	J. and Sugiyama, T. 1 (FKHL 14) mesenchyme fork sir gene and protein	4
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Miura,N.
Direct Submission
Submitted (18-SEP-1996) N. Miura, Akita University School of
Medicine, Department of Biochemistry, 1-1-1 Hondo, Akita 010, JAPAN
Location/Qualifiers
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Homo sapiens chromosome 16 clone RP11-46309, complete sequence.
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DDE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
Direct Submission Submitted (29-CCT-2002) DDE Joint Genome Institute, 2800 Mitchell Submitted (29-CCT-2002) DDE Joint Genome Institute, 2800 Mitchell Only walnut Creek, CA 94598, USA on Oct 29, 2002 this sequence version replaced gi:13786306.
Draft Sequence Produced by DOE Joint Genome Institute
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National Laboratory
www-shgc.stanford.edu
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarihini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               721 AGCGGGGCCGCCGCCTGCCCTGCCCGGGCGCGCCCTCCAGGATGCCGATCCGCCCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCGGGCCGGCGCTGCCCTTGCCCGGGGCGCGCCCTCCAGGATGCCGATCCGCCCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1052 Adecraccadadadecededecedecerecederecerrecrererecereradearerer
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692 AACTITICCCAATCCCTAAAAGGGACTIGGCCTCTTTTTCTGGGCTCAGCGGGGCAGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  781 CGCIGAAAGCGCGCCCCCTGCTCGGCCCCGACGACGACGACGACGCACCGCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 752 CICGACCCGGGGGGGCGTGACCTGGGGGCTGCCGATTCGCTGGGGGCTTGGAGAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 168656)
DOE Joint Genome Institute, Stanford Human Genome Center and
Alamos National Laboratory.
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Estimated Total Number of Errors is 0.2.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1172 GCCGGCGAGCCGTCTCGGAAGCAGCA 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961 GCCGGCGAGCCGTCTCGGAAGCAGCA 986
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DOE Joint Genome Institute.
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APPLICANT: LYAIN DOUGETES-Stamm et al
APPLICANT: LYAIN DOUGETES-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
                                                    Gaps
                                                    ó
100.0%; Score 12; DB 3; Length 361; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 12; DB 4; Length 535; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 12; DB 4; Length 381; 100.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JOBERT, S.
APPLICANT: Glordano. J.Y.
TITLE REPRENCE: GENOST: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9538
IRDGTH: 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                        Sequence 1782, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-621-976-9538; Application US/09621976; Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 7, Application US/09918686
; Patent No. 6475739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Enterococcus faecalis
US-09-134-000C-1782
Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               513 GGAAGTAAAA 524
                                                                                                                                                  112 GGAAAGTAAAAA 101
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                                                                                                   1 GGAAAGTAAAA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-9538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 12; Conserv
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LENGTH: 381
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GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
IIILE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
CURRENT APPLICATION NUMBER: US 09/671,317
CURRENT APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION.

APPLICANT: ATV. I Breton et al.

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTS-09-03PB.

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILLING DATE: 1999-06-04
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Peeper, Bryan
APPLICANT: Staehling-Hampton, Karen
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: GETHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REPRENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT APPLICATION NUMBER: 2001-07-30
CURRENT PILING DATE: 2001-07-30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 429, Application US/09671317
Patent No. 6528260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-328-352-713
; Sequence 713, Application US/09328352
Patent No. 6563958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 GGAAAGTAAAA 332
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SEQ ID NO 713
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Best Loca
Matches
                                                                                                     APPLICANT: Oefner, Peter J.
APPLICANT: Underhill, Peter A.
APPLICANT: Underhill, Peter A.
APPLICANT: Underhill, Peter A.
TITLE OF INVENTION: Detection of DNA Heteroduplex Molecules
TITLE OF INVENTION: by Denaturing High Performance Liquid Chromatography and
TITLE OF INVENTION: Methods for Comparative Sequencing
TITLE OF INVENTION: Methods for Comparative Sequencing
TORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A NOVEL FAMILY OF HIGH AFFINITY, MODIFIED ANTIBODIES FOR CANCER TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 9; DB 1; Length 22; 100.0%; Pred. No. 2.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PTLING DATE:
CLASSIPICATION NUMBER: US/08/512,681
FILING DATE:
CLASSIPICATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 8600-0155
REFERENCE/DOCKET NUMBER: 8600-0155
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 25 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA

/ ORIGINAL SOURCE:
// INDIVIDUAL ISOLATE: DYS234 REVERSE PRIMER
US-08-512-681-19
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Patent No. 5993813
GENERAL INFORMATION
APPLICANT: (MEZES, PETER S
APPLICANT: GOUNTLE, BRIAN B
                                          Sequence 19, Application US/08512681
Patent No. 5795976
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDERSON, WH KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLOM, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A NOVEL TITLE OF INVENTION: MODIFIED NUMBER OF SEQUENCES: 74 CORRESPONDENCE ADDRESS: DUANE C ULMER STREET: P.O. BOX 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIXON, MARK W
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACAAATGTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 ACAAATGTT 6
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                                                                                                                                                                                                                                                                                                                                                                     USA
RESULT 11
US-08-512-681-19/c
                                                                                                                                                                                                                                                                                                                                                                                         94306
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                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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APPLICANT: BERGERON, Michel G.
APPLICANT: BERGERON, Francois J.
APPLICANT: PIGARD, Francois J.
APPLICANT: PIGARD, Francois J.
APPLICANT: POSTILETE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ... NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 100.0%; Score 9; DB 2; Length 22; Local Similarity 100.0%; Pred. No. 2.8e+03; nes 9; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
PEPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIPICATION: 435
PRICR APPLICATION DATA:
PRILICATION: WIMBER: US/08/526,840
FILING DATE: 1-SEP-1995
ATORNEY/AGENT INFORMATION:
NAME: BARES Jean C.
NAME: BARES Jean C.
NAME: RAFER Jean C.
NAME: CATERALION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85,686,90012
                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: ULAKEN, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMULICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 411 EAST WISCONSIN AVENUE
MILWAUKEE
WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 240, Application US/08743637B Patent No. 5994066 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 ACAAATGTT 20
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                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
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US-08-743-637B-240/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-822-028-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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March 25, 2004, 10:03:04; Search time 14.7262 Seconds (without alignments) 4297.861 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09E_NEW PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09E_NEW PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2458946 seqs, 1861504846 residues
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1 tgtggaaggaataaata 17
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Maximum Match 100%
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		ID Description	3 US-10-027-632-9718 Sequence 9718, Ap	US-09-963-285-1 Sequence 1, Appli	2 US-10-424-599-107702 Sequence 107702,	3 US-10-424-599-82796 Sequence 82796, A	US-09-764-891-10003 Sequence 10003, A	1 US-10-205-428-977 Sequence 977, App	s US-10-131-827-1138 Sequence 1138, Ap	2 US-10-424-599-64036 Sequence 64036, A	0 US-09-814-353-17187 Seguence 17187, A	2 US-10-424-599-22032 Sequence 22032, A		US-10-027-632-242034	12 US-10-424-599-141232 Sequence 141232,	2 US-10-424-599-63676 Sequence 63676, A	5 US-10-027-632-148185 Sequence 148185.
		Match Length DB	962 1	6458 9	493 13	2523 13	21619 10	21619 14	50 1	359 1	386	493 1	589		606 1	616 1	676 1
	* Query	Match	100.0	100.0	94.1	94.1	94.1	94.1	90.6	90.6	9.06	9.06	9.06	9.06	9.06	90.6	90.6
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Length 962; Indels

Query Match
100.0%; Score 17; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 0;

1 TGTGGAAGGAATAAATA 17

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Sequence 37752, A Sequence 4341, A Sequence 256264, Sequence 256264, Sequence 256264, Sequence 25, Appl Sequence 12, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 1311, Appl Sequence 1314, Appl Sequence 1367, Appl Sequence 1367, Appl Sequence 1367, Appl Sequence 1369, Appl Sequence 14, Appli Sequence 14, Appli Sequence 17, App	le Nucleotide
2 US-10-424-599-37752 2 US-10-424-599-43641 5 US-10-027-632-2566263 5 US-10-027-632-256264 4 US-10-106-698-95 5 US-10-027-632-256264 5 US-10-027-632-256264 6 US-10-027-4177-12 5 US-10-229-345-12 5 US-10-24-177-12 5 US-10-24-177-12 5 US-10-26-64-2121 6 US-10-29-96-27 7 US-10-21-613-351 4 US-10-21-613-351 4 US-10-21-613-351 4 US-10-21-613-85 6 US-10-21-613-85 7 US-10-21-613-85 8 US-10-02-154-1369 8 US-10-09-154-1369 8 US-10-09-154-1369 9 US-10-09-154-1369 1 US-10-09-164-1369 1 US-10-09-164-1369 1 US-10-09-164-1369 1 US-10-09-164-1369 1 US-10-09-164-186-9	ALIGNMENTS //0027632 A9
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US-09-963-285-1

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Sequence 82796, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: Lar Rosa Thomas J
APPLICANT: Lar Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5323) B/10/424,599
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 82796
LENGTH: 2523
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; Publication No. US2033077808A1
; Publication No. US2033077808A1
; GENERAL INFORMATION:
; APPLICAT'R ROSen et al.
; TITLE OF INVENTION: NUMBER: US/09/764,891
; CURRENT APPLICATION UNMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper: NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10003
; LENGTH: 21619
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US-10-424-599-82796
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2 GTGGAAGGAATAATA 17
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Matches 16; Conservative
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Sequence 10702, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: DATE: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 107702
LINGTH: 493
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OTHER INFORMATION: unsure at all n locations
FBATURE:
                                                                                                            US-09-963-288-1

SQUENCE 1, Application US/09963285

Patent No. US20020090707AL

GENERAL INFORMATION:

APPLICANT: Enerbock, Sven

APPLICANT: Krook, Katarina

APPLICANT: Rondahl, Weth

TITLE OF INVENTION: PROMOTER SEQUENCES

FILE REPRESENCE: 13425-04201

CURRENT APPLICATION NUMBER: US/09/963,285

CURRENT FILING DATE: 2001-09-26

PRIOR FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: US 60/238,897

PRIOR APPLICATION NUMBER: US 60/238,897

PRIOR APPLICATION NUMBER: SE 0004102-0

PRIOR PLING DATE: 2000-10-0

PRIOR PLING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 24

SSOTHARE: PASCESO for Windows Version 4.0

SEQ ID NO!

LENGTH: 6458
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; LOCATION: (2235)...(3737)
US-09-963-285-1
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Best Local Similarity
Matches 17; Conserv
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NAME/KEY: unsure
LOCATION: (1)..(4
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TYPE: DNA

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Sequence 977, Application US/10205428
Fublication No. US20030108907A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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Query Match 94.1%; Score 16; DB 12; Length 493; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 16; Conservative 0; Mismatches 0; Indels

; OTHER INFORMATION: Clone ID: PAT_MRT3847_68271C.1 US-10-424-599-107702

TYPE: DNA

US-10-205-428-977/c

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

March 25, 2004, 08:39:03; Search time 81.7624 Seconds (without alignments) 6361.316 Million cell updates/sec Run on:

US-09-963-285-1_COPY_1692_1703 Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3470272 segs, 21671516995 residues Searched:

6940544 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

em_hum:* em_in:* em_mu:* em pat:* em_om:* em sts: em ov:*

Pred. No. is the number of results predicted by chance to have a em_htgo_mus:* em_htgo_other:* em_sy: em_htgo_hum:*

em_htg_vrt:*

em_htg_inv:*
em_htg_other:*
em_htg_mus:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence	BD273541 Recombina	AR267926 Sequence	AF227460 Bromus te	AX305717 Sequence	G55264 SHGC-100532	AX909385 Sequence	AJ578474 Brassica	AL009426 H.sapiens	AF184852 ATADIACDS AU046405 Rattus no	G74846 STS6-204 Sm	01831/ Bacillus su AJ431205 Nicotiana	AF288758 Cryptobia BY322133 Arahidons	AY019564 Oryza sat	BX322076 Arabidops BX322104 Arabidops	BD058786 Secreted	X15668 Homo sapien AJ594039 Arabidops	AJS98168 Arabidops	GZ3240 numan SIS W AY036343 HIV-1 iso	Z51097 H.sapiens (G36089 STS A14A173 AJ588365 Arabidops	AX910794 Sequence	BD046327 Sequence AB043926 Homo sapi	AB043909 Homo sapi	AB043910 Homo sapı AB043911 Homo sapi	AB043932 Homo sapi	AB043939 Homo sapi AB043942 Homo sapi	BD204302 5'EST and	AB073287 Macaca fu AL807135 Arabidops	X17266 Zebrafish ĥ		E	inear FAI 07-0CI-159			and Clouthier, S.C.		
SUMMARIES	Q	144897 NO147023	BD273541	AR267926	AF227460	AX305717	BA34143 G55264	AX909385	BNA578474	HSPE10B10	AF184852 AU046405	G74846	U1831/ NOT431205	AF288758	AY019564	BX322076 BX322104	BD058786	HSY15668 AJ594039	AJ598168	GZ3240 AY036343	HS189XB6	G36089 AJ588365	AX910794	BD046327 AB043926	AB043909	AB043910 AB043911	AB043932	AB043939 AB043942	BD204302	AB073287 AL807135	BRHOX61	ALIGNMENTS		19 DP DNA ent US 5635617.			, Collinson, S. Karen.	34 03=:TIN-1997;	6T-NOOLCO #6
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 12; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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            /organism='Unidentified'
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—Aneressed production of interferon—g(a)
Patent: WO 0118039-A 2 15-MAR-2001;
GLAXO GROUP LIMITED (GB)
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Cochran,M.D. and Junker,D.E.
Recombinant swinepox virus
Patent: US 6497882-A 265 24-DEC-2002;
Location/Qualifiers
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Sequence 265 from patent US 6497882.

    .58
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    .28
    /organism="unidentified"
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    /db_xref="taxon:32644"

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Sequence 2 from Patent WO0118039.
AX093873 GI:13510091
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/wol_type="genomic DNA"
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01-MX-1999 US 09/017111
BARRARA J WINSLOW MARK D COCHRAN
CIRNIS/09,A61K39/12,A61K39/125,A61K39/15,A61K39/23,
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Winslow, B.J. and Cochran, M.D.
Recombinant virus expressing foreign DNA encoding feline CD80,
feline CD86, feline CTLA-4 or feline interferon-gamma and uses
Patent: JP 2002513581-A 75 14-MAY-2002;
SCHERING-FLOUGH LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD273541 28 bp DNA linear PAT 17-JUL-Recombinant virus expressing foreign DNA encoding feline CD80, feline CD86, feline CTLA-4 or feline interferon-gamma and uses
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PC A61K48/00,A61P43/00,C12N7/00//C07K14/705,C12N15/00 CC PPR downstream primer.
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0
                                                                                             100.0%; Score 12; DB 6; Length 19; 100.0%; Pred. No. 5.9e+04; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 28)
Cochran, M.D. and Junker, D.E.
Recombinant swinepox virus
Patent: US 6221361-A 84 24-APR-2001;
Location/Qualifiers
               1. .19
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                           AR147023 28 bp 1
Sequence 84 from patent US 6221361.
AR147023.1 GI:15110826
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/organism="unknown"
/mol_type="unassigned DNA"
Location/Qualifiers
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JP 2002513581-A/75
14-MAY-2002
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BD273541.1 GI:33083309
JP 2002513581-A/75.
unidentified
                                                                                             Query Match
Best Local Similarity 100.
Matches 12; Conservative
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AR147023/c
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BD273541/c
LOCUS
DEFINITION
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Submitted (31-MAR-2003) Clarke J.H., John Innes Centre, Colney Submitted (31-MAR-2003) Clarke J.H., John Innes Centre, Colney Jane, Norwich, NR4 7UJ, UK and denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MR a defective suppressor minator transposon. 3 denotes a sequence derived from the 3'end of the transposon BRBRC GARNAC, ATIS project Continue seed stock requests: http://nasc.nott.ac.uk/ NASC stock
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                                                                                                                                                BX322143 19-JUN-2003
Arabidopsis thaliana transposon insertion STS SM_3.35925, sequence
                                                                                                                                                                                                                                                          STS; STS, sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 206) Olivier, M. and Cox, D.R. (2000) Unpublished, Olivier, M., Cox, D.R. (2000)
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G55264
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/mol type="genomic DNA"
/wol type="genomic DNA"
/wariety="Columbia-0 NASC stock code N1092"
/db xref="taxon:3702"
/clone="Ac006841"
/note="Derived from superpool 25.06 NASC code N41149"
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                                                                                                                                                                                                                                                                                                                                                                                                               Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B.,
Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
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    191
    standard_name="SM_3.35925"

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Homo sapiens
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Unpublished
2 (bases 1 to 191)
                                   102 GGAAGTAAAA 113
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1 GGAAAGTAAAA 12
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                                                                                                                                                                                             tagged site.
BX322143
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Best Local Similarity
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G55264/c
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                                                                                                                                                     linear PLN 13-JUN-2000
                                                                                                                                                                                                                                                                                  Bromus tectorum

Bromus tectorum

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Bromeae, Bromus.

1 (bases 1 to 150)
Paulsen, A., Meyer, S.E., Coleman, C.E. and Fairbanks, D.J.

Microsatellite markers for Bromus tectorum (cheatgrass)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 150)
Paulsen,A., Meyer,S.E., Coleman,C.E. and Fairbanks,D.J.
Paulsen,A., Meyer,S.E., Coleman,C.E. and Fairbanks,D.J.
Direct Submission
Submitted (21-JAN-2000) Botany and Range Science, Brigham Young University, 401 WIDB, Provo, UT 84602, USA
Location/Qualifiers
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Patent: WO 0188188-A 468 22-NOV-2001;
School Juridical Person Nihon University (JP)
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                                                                                                                                      150 bp DNA linear
Bromus tectorum clone 21 microsatellite sequence.
AF227460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bromus tectorum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX305717
Sequence 468 from Patent WO0188188.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:29667"
/clone="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="microsatellite"
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  1 GGAAAGTAAAA 12
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PAT 27-AUG-2002

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Gaps

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Divaryota; Eucheria; Craniata; Vertebrata; Euteleostomi; Bukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Hoases 1 to 207)

E dwards,J.B.D.M., Duclair,E. and Jordan,J.Y.

Sequence tag and encoded human protein

Patent: JP 2001269182-A 21164 02-OCT-2001;

GENSET

OS Homo sapiens (human)

PN JP 2001269182-A/21164

PD 02-OCT-2001

PP 24-FEB-2000 JP 2000118773

PR 26-FEB-1999 US 60/122487

PI JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES

PI JORDAN

PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica napus chloroplast partial psbC gene for PSII 43 kDa protein, IGS and partial tRNA-Ser (UGA) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C12N5/10,
PC C12R21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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AJ578474.1 GI:37992039
IGS, intergenic spacer; psbC gene; PSII 43 kDa protein; transfer RNA-Ser (UGA); tRNA-Ser (UGA) gene.
chloroplast Brassica napus (rape)
Brassica napus (Brighlantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; resids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                     Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 207;
                                                                     Query Match 100.0%; Score 12; DB 6; Length 20 Best Local Similarity 100.0%; Pred. No. 4.1e+04; Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.1e+04;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                           Sequence tag and encoded human protein.
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                        BD044918.1 GI:22586660
JP 2001269182-A/21164.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                     79 GGAAAGTAAAA 90
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BD044918
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAC ends sequenced at TIGR from the RPCIII BAC library. Designed and developed at the Stanford Human Genome Center. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                      Initial incubation: 95 degrees C for 10 minutes Denaturation: 94 degrees C for 30 seconds Annealing: 60 degrees C for 30 seconds POLYMerization: 72 degrees C for 23 seconds PCR Cycles: 70 Perkin Elmer 9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
        Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5801
Fax: (650) 320-5801
Email: olivierSebgc.stanford.edu
Primer A: TCACTTAACTTTGCGAACCCATT
Primer B: CTAGTGTTTGCTTCCCTTCCCT
FCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 25248 06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

100.0%; Score 12; DB 11; Length 206;
Best Local Similarity 100.0%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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each 1 uM
each 200 uM
0.07 units/ul
5 ul
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Organism="Homo sapiens"
Mol type="genomic DNA"
/db xref="taxon:9606"
/map="14"
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Total Vol:
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/organism="Homo sapiens"
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50 mM
10 mM
8.3
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complement(123.'.145)
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19. .145
                                                                                                                                                                                                                                              Denaturation:
Annealing:
Polymerization:
PCR Cycles:
Thermal Cycler:
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Homo sapiens
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Tris-HCl:
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dNTPs:
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primer_bind
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COMMENT
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Gaps

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Direct Submission
Submitted (25-JUL-2003) Day A., School of Biological Sciences,
University of Manchester, 3.614 Stopford Building, Oxford Road, M13
9PT, UNITED KINGDOM
Location/Qualifiers
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I (bases I to 210)

Gragory, S., Kettleborough, R., Langford, C., Ross, M.T. and Hunt, S.E. Direct Submission

Submitted (03-DEC-1997) E-mail contact: humquery@sanger.ac.uk
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Zubko,M.K., Zubko,E.I., van Zuilen,K., Meyer,P. and Day,A.
Stable plastid transformation of Petunia plastids
Unpublished
2 (bases 1 to 209)
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                                                                                                                                                                                                                                                                                                                                                                                               /function="photosynthetic protein"
/codon start=1
                                                                                                                                                                                                                   /organism="Brassica napus"
/organelle="plastid:chloroplast"
/mol_type="genomic DNA"
/cultivar="naxs"
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/product="PSII 43 kDa protein"
/protein.id="CAB18106.1"
/db xref="GI:37992040"
/translation="MTPLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19, .193
/note="intergenic spacer, IGS"
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/gene="tRNA-Ser (UGA)"
complement (194, >209)
/gene="tRNA-Ser (UGA)"
/product="tRNA-Ser"
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                              /db_xref="taxon:3708"
1. .18
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STS; single read.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                      'gene="psbC"
                                                                                                                                                                                                                                                                                                                                                                          "gene="psbc"
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AL009426
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                                                                                   Day, A.
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AU046405 22-APR-1999 DNA linear STS 22-APR-1999 Rattus norvegicus, OTSUKA clone, 01478, microsatellite sequence, sequence tagged site.
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AFabidopeis thaliana inhibitor tagged site ITS85 genomic sequence.
AF184852.1 GI:6272782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Manoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 229)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spellman, E., Metz, P.L., van Arkel, G., te Lintel Hekkert, B., Stiekema, M.J. and Pereira, A. A. two-component enhancer-inhibitor transposon mutagenesis system for functional analysis of the Arabidopsis genome Plant Cell 11 (10), 1853-1866 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Speulman, B., Metz, P.L.J., van Arkel, G., te Lintel Hekkert, B., Stiekema, W.J. and Pereira, A.
Direct Submission.
Submitted (11-SEP-1999) Molecular Biology, CPRO-DLO, P.O. Box 16, Wageningen 6700AA, The Netherlands
Location/Qualifiers
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0
                                                                                                                                           100.0%; Score 12; DB 11; Length 210; 100.0%; Pred. No. 4.1e+04; ative 0; Mismatches 0; Indels C
                                  /tissue type="BBV lymphoblastoid cell line"
/clone_lib="SC1pE"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 12; DB 8; Length 229; 100.0%; Pred. No. 4e+04; ative 0; Mismatches 0; Indels
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/organisme"Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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Rattus norvegicus
'clone="SClpEl0Bl0"
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                      /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 229)
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                                                                                                                                                                                         12; Conservative
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Best Local Similarity
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1 (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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Watanabe, T.K., Hishigaki, H., Okuno, S., Mizoguchi, A., Oga, K., Tsuji, A., Ono. T., Yamasaki, Y., Kanemoto, N., Takahashi, E., Irie, Y., Tsuji, A., Ono. T., Yamasaki, Y., Kanemoto, N., Takahashi, E., Irie, Y., The large-scale mapping of rat microsatellite markers

L. Unpublished

E. (Dassel to 247)

Watanabe, T.K.

Direct Submission

L. Submitted (11-DEC-1998) Takeshi K Watanabe, Otsuka GEN Research
Institute, Otsuka Pharmaceutical Co., Ltd; 463-10, Kagasuno,
Kawanchi-cho, Tckushima, Tokushima 771-0192, Japan
(E-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888,
Fax:+81-886-37-1035)
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/mol_type="genomic DNA"
/srzafin="Brown Norway"
/db xrsef="taxon:10116"
/clone="01478"
/cell_type="hepatocyte"
/issue_type="liver"
/note="01478F=5'-TCACATCCACCATCCTCAAAT-3',
01478R=5'-ACAACTTATTACCTGCCCAGACC-3'"
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Search completed: March 25, 2004, 12:49:42 Job time : 85.7624 secs

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Sequence 1 Patent No. Sequence 1

US-10-079-616-5 US-10-079-616-5 US-09-873-404-1 Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence

US-08-811-682-14 US-08-857-076-43 US-08-11-681-632 US-08-221-0178-632 US-08-25-171E-186 US-08-95-171E-186 US-08-95-547-9 US-08-315-547-9 US-09-946-239-7 US-09-946-239-7 US-09-946-239-7 US-09-946-239-7 US-09-946-239-7 US-09-946-239-7 US-09-946-239-7 US-09-946-239-7 US-09-946-239-7 US-09-946-239-7

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Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 1782, Ap
Sequence 7, Appli
Sequence 7, Appli
Sequence 713, Appli
Sequence 429, Appli
Sequence 429, Appli
Sequence 429, Appli
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                                                          March 25, 2004, 09:55:14; Search time 2.36035 Seconds (without alignments) 2821.370 Million cell updates/sec
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Sequence 49,
Sequence 1, A
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Sequence 2
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                                                                                                                                                                                                                                                                       /cgn2_6/ptcdata/2/ina/5A_COMB.seq:*
/cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-233-788A-34
US-08-686-968C-84
US-08-472-679H-265
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                                                                                                                                                               682709 segs, 277475446 residues
                                                                                                 US-09-963-285-1_COPY_1692_1703
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Maximum Match 100%
Listing first 45 summaries
                                            nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 12; DB 3; Length 28; 100.0%; Pred. No. 1.1e+03; ive 0; Mismatches 0; Indels
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/ Sequence 265, Application US/08472679H

/ Sequence 265, Application US/08472679H

/ GENERAL INFORMATION:

/ APPLICANT: Cochran, Mark D.

/ TITLE OF INVENTION: Recombinant Swinepox Virus

// NUMBER OF SEQUENCES: 267

// CORRESPONDENCE ADDRESS:

// CORRESPONDENCE ADDRESSE:

// STREET: 2000 Galloping Hill Road
                                                                                          APPLICANT: Junker, David E.
TILE OF INVENTION: Recombinant Swinepox Virus
FILE REFERNCE: 39119-H/JML US/08/686,968C
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 84
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEPAX: (908) 298-3388
INFORMATION FOR SEQ ID NO: 265:
SEQUENCE CHARACTERISTICS:
                        Application US/08686968C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
                                                                               Jochran, Mark D.
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAAAGTAAAA 12
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              US-08-686-968C-84/c
RESULT 2
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APPLICANT: Winelow, Barbara J.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CTLA-4 or
TITLE OF INVENTION: Feline Interferon-gama And Uses Thereof
FILE REFERENCE: 54957-B
CURRENT APPLICATION NUMBER: US/09/303,040
CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 60/083,870
EARLIER APPLICATION NUMBER: 60/083,870
EARLIER APPLICATION NUMBER: 00/083,870
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 80
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GENERAL INFORMATION:
TITLE OF INVENTION: WOULD HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: WOULD HUMAN GENES
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT TILING DATE: 1999-08-30
EAALIER PILING DATE: 1999-06-08
EAALIER PILING DATE: 1999-01-27
EAALIER APPLICATION NUMBER: 60/117,393
EAALIER APPLICATION NUMBER: 60/117,393
EAALIER PILING DATE: 1999-01-27
SARLIER PILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 544-08-31
NUMBER OF SEQ ID NOS: 544-08-31
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 361
                                                                                               100.0%; Score 12; DB 4; Length 28; 100.0%; Pred. No. 1.18+03; tive 0; Mismatches 0; Indels
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Conservative 0: Mismath. 1.1.16+03;
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-08-472-679H-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA; TYPE: DNA; OKGANISM: FIV PPR downstream primer US-09-303-040-80
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US-09-385-982-26/c
; Sequence 26, Application US/09385982
==-ant No. 6262334
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; Sequence 80, Application US/09303040

; Patent No. 6555671

; GENERAL INFORMATION:
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) LOCATION: (1)...(361)
) OTHER INFORMATION: n = A,T,C or G
                                                                                                                    Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                              27 GGAAAGTAAAA 16
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
                                                                                                    Query Match
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Sequence 1782, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUMBER: US/09/134,000C

CURRENT PELICATION NUMBER: US 60/055,778

PRIOR APPLICATION UNDER: US 60/055,778

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PATENT VERSION 3.1

SEQ ID NO 1782

LENGTH: 381
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100.0%; Score 12; DB 4; Length 381;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels
                   Length 361;
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jubert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REFERENCE: GENEET, 054PR2; CURRENT APPLICATION NUMBER: US/09/621,976; CURRENT PILING DATE: 2000-07-21; NUMBER OF SEQ ID NOS: 19335; SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 12; DB 4; I
100.0%; Pred. No. 1.1e+03;
:ive 0; Mismatches 0;
              Query Match
100.0%; Score 12, DB 3; 1
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
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Patent No. 6475739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecalis
US-09-134-000C-1782
                                                                                                                                                      112 GGAAAGTAAAAA 101
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Best Local Similarity 100.
Matches 12; Conservative
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; ORGANISM: Homo sapiens
US-09-621-976-9538
                                                                                                                                                                                                                     RESULT 6
US-09-134-000C-1782/c
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US-09-621-976-9538
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US-09-918-686-7
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Sequence 429, Application US/09671317

Sequence 429, Application US/09671317

Patent No. 6528260

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta
APPLICANT: Cham. Annick
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFERENCE: 62.083.CIP
FILE OF INVENTION NUMBER: US/09/671,317
CURRENT APPLICATION NUMBER: US/09/671,317

PRIOR FILING DATE: 2000-03-23
FRIOR FILING DATE: 2000-03-23
FRIOR FILING DATE: 2000-03-24

FRIOR APPLICATION NUMBER: US 60/126,269
FRIOR FILING DATE: 1999-03-25
FRIOR FILING DATE: 1999-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: GETOT. Breton et al.
TITLE OF INVENTION: ACCETEC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
SEQ ID NOS: 8252
LENGTH: 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 12; DB 4; Length 602; 100.0%; Pred. No. 1.1e+03; ive 0; Mismatches 0; Indels
APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Paceper, Bryan
APPLICANT: Stachling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFURMER: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 713, Application US/09328352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
, ORGANISM: Acinetobacter baumannii
US-09-328-352-713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 GGAAAGTAAAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 GGAAAGTAAAA 332
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                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-686-7
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US-09-671-317-429
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us-09-963-285-1_copy_1692_1703.rni

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| Sequence 524, Application US/09641638 |
| Sequence 524, Application US/09641638 |
| Patent No. 6432646 |
| General Incomatron |
| APPLICANT: Blumenfeld, Marta |
| APPLICANT: Bougueleret, Lydie |
| APPLICANT: Chumakov, Ilya |
| APPLICANT: Chumakov, Ilya |
| APPLICANT: Chumakov, Ilya |
| TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING |
| TITLE OF INVENTION: GENEST: 08/09/641, 638 |
| TITLE OF ILLING DATE: 2000-08-16 |
| CURRENT APPLICATION NUMBER: US/09/641, 638 |
| PRIOR APPLICATION NUMBER: US 09/502,330 |
| PRIOR FILING DATE: 2000-02-11 |
| PRIOR APPLICATION NUMBER: US 60/133,200 |
Sequence 875, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDERSS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
COUNTRY: DALO ALFO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 12; DB 4; Length 966; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURENY APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATA:
APPLICATION NUMBER:
FILING DATA:
FRIGHT ON NUMBER:
FILING DATE:
FILING
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NAME: Zeller, Karen J.
REGISTRATION UNDHER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEFAN: (650) 845-4166
INFORMATION FOR SEQ ID NO: 875:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYRE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 GGAAAGTAAAAA 260
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CLONE: 91088447
US-09-023-655-875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-641-638-524
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US-09-114-000C-701/C

J SQUENCE 701, Application US/09134000C

REQUENCE 701, Application US/09134000C

REQUENCE 701, Application US/09134000C

RECORDERAL INFORMATION:

APPLICANT NON.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 701

LENGTH: 732

LENGTH: 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

FEATURE:

FEATURE:

FAME/KEY: allele

LOCATION: 364

OTHER INFORMATION: 12-622-325: polymorphic base C or T

NAME/KEY: misc_binding

LOCATION: 344.363

OTHER INFORMATION: 12-622-325.misl, potential

NAME/KEY: misc_binding

LOCATION: 355.384

OTHER INFORMATION: 12-622-325.mis2, potential complement

NAME/KEY: primer_bind

LOCATION: 351.366

OTHER INFORMATION: upstream amplification primer

NAME/KEY: primer_bind

LOCATION: 351.366

OTHER INFORMATION: downstream amplification primer, complement

NAME/KEY: misc_binding

LOCATION: 352.376

OTHER INFORMATION: 12-622-325 potential probe

NAME/KEY: misc_feature

LOCATION: 33,865.688

COTHER INFORMATION: 12-622-325 potential probe

NAME/KEY: misc_feature

COTHER INFORMATION: 12-622-325 potential probe

NAME/KEY: misc_feature

COTHER INFORMATION: 12-622-325 potential probe

COTHER INFORMATION: 12-622-325 potential probe

COTHER INFORMATION: 12-622-325 potential probe

COTHER INFORMATION: 12-622-325 potential probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 12; DB 4; Length 732; 100.0%; Pred. No. 1.1e+03;
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                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SOFTWARE: Patent.pm
SEQ ID NO 429
LENGTH: 710
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; ORGANISM: Enterococcus faecalis
US-09-134-000C-701
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
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Gaps

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RESULT 12 US-09-023-655-875

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Gaps
                                                              NAME/KEY: misc_binding

LOCATION: 502..521

OTHER INFORMATION: 10-298-158.mis2, potential complement

NAME/KEY: primer_bind

LOCATION: 348..365

OTHER INFORMATION: upstream amplification primer

NAME/KEY: primer_bind

LOCATION: 770..789

OTHER INFORMATION: downstream amplification primer, complement

NAME/KEY: misc_binding

LOCATION: 489..513

OTHER INFORMATION: 10-298-158 potential probe

US-09-641-638-525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: May, LUMINIS
APPLICANT: Wang, Dunrul
APPLICANT: Wang, Zhiwei
APPLICANT: Under Tillinghast
APPLICANT: Under Tillinghast
APPLICANT: Under Tillinghast
TITLE OF INVENTION: Do'Lyoptides
FILE OF INVENTION: Do'Lyoptides
FILE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312B
CURRENT APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PF. FL. Genes Version 1.0
SEQ ID NO 202
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 12; DB 4; I Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 12; Conservative 0; Mismatches 0;
                                LOCATION: 481. 500
OTHER INFORMATION: 10-298-158.mis1, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-620-312D-203
; Sequence 203, Application US/09620312D
; Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, vinod
APPLICANT: Cheng, Jie
APPLICANT: Chen, Peiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: And, Qing A.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Wen, Suchong
APPLICANT: Wang, Jian-Rui
APPLICANT: Ang, Yonghong
APPLICANT: Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539 GGAAAGTAAAAA 550
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ma, Yunging
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; LOCATION: (93)..(1082)
US-09-620-312D-203
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APPLICANT: Blumenfeld, Marta
APPLICANT: Bouqueleret, Lydie
APPLICANT: Bouqueleret, Lydie
APPLICANT: Bouqueleret, Lydie
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 10ya
TITLE OF INVENITON: BIALIELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENITON: GENER: US/09/641,638
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
FRIOR FILING DATE: 1000-08-16
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SEQ ID NO 525
LEAGTH: 1001
TARGOTH: 1001
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                                                                                                                                                                                                                                                                                                    NAME/KEY: allele

LOCATION: 501

OTHER INFORMATION: 10-298-122 : polymorphic base C or T
NAME/KEY: misc_binding
LOCATION: 481.500

COTHER INFORMATION: 10-298-122.misl, potential
NAME/KEY: misc_binding
LOCATION: 502.521

COTHER INFORMATION: 10-298-122.misl, potential complement
NAME/KEY: primer_bind
LOCATION: 384.401

COTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 806.436

COTHER INFORMATION: 000-0386

LOCATION: 489.513

COTHER INFORMATION: 10-298-122 potential probe
USC-09-641-638-524
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 10-298-158 : polymorphic base A or G
| PRIOR FILING DATE: 1999-05-07 | PRIOR APPLICATION NUMBER: US 09/275,267 | PRIOR PILING DATE: 1999-03-23 | PRIOR PILING DATE: 1999-02-12 | PRIOR FILING DATE: 1999-02-12 | NUMBER OF SEQ ID NOS: 1304 | SOFTWARE: Patent.pm | SSEQ ID NO 524 | LENGTH: 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 525, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575 GGAAAGTAAAA 586
                                                                                                                                                                                                                                                           ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                     TYPE: DNA
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Search completed: March 25, 2004, 15:34:19 Job time : 4.36035 secs

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GenCore version 5.1.6
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OM nucleic - nuc	nucleic E	search, using sw model
Run on:	March	39:03 ; Search
		(without alignments) 6361.316 Million cell updates/sec
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	1 ctga	ctgccattccaatccagcgcgagccgtctcggaagcagca 986
Scoring table:	IDENTI Gapop	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272	2 seqs, 21671516995 residues
Total number of	hits	satisfying chosen parameters: 6940544
Minimum DB seq 1 Maximum DB seq 1	ength:	2000000
Post-processing:	Minimum Maximum Listing	num Match 0% num Match 100% ng first 45 summaries
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		m_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query	Length	DB	QI	Description
	86	8	328	6	SMFH	223 H.sapien
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m	298.	30.3		10	AC127554	127554 Mus
4	29	29.4		10		222 M.musc
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28	75.		8176	C)		29 Homo
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	74.	•		11	2A1	34286 Penici
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	7			N	101	1017 Homo sa

PRI 14-MAY-1997		teleostomi; Iomo.	.,T. enchyme fork otein
linear PF	gene .	. Vertebrata; Eu ii; Hominidae; E	.L. and Sugiyams nn (FKHL 14) mes heir gene and pr
3289 bp DNA	rotein; MFH-1 g	data; Craniata; ates; Catarrhir	uma,H., Yang,X. MFH-1) and huma servation of th
HSMFH1 H capione MFH-1 Gene	n. Sapless Mrn. 1 gene. Y08223. Y08223.1 G1:1869804 mesenchyme fork head-1 protein, MFH-1 gene. Homo saplens (human)	Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.	Miura,N., Iida,K., Kakinuma,H., Yang,X.L. and Sugiyama,T. Isolation of the mouse (MRH-1) and human (FKHL 14) mesenchyme fork head-1 genes reveals conservation of their gene and protein
RESULT 1 HSMFH1 LOCUS	ACCESSION VERSION KEYWORDS	ORGANISM	REFERENCE AUTHORS TITLE

ALIGNMENTS

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Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
National Laboratory
www-shgo.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
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DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Submitted (29-OCT-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Oct 29, 2002 this sequence version replaced gi:13786306.

Draft Sequence Produced by DOE Joint Genome Institute
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DOE Joint Genome Institute.
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/db_xref="G1:1869805"

/db_xref="G0A:09958"

/db_xref="GNA:S-PROT:099958"

/db_xref="GNA:S-PROT:099958"

/bc_xref="GNA:S-PROT:099958"

/cranslation="MQARYSVSDPNALGVVPYLSEQNYYRAAGSYGGMASPMGVYSGH

PROYSAGMARGRYAPYHHUAPAAPACLVXPPYDAXTALTMYATATLNATYGFI

MDRPPPYRENKQGMONSIRHNI.SLNSCPWYRVBXDDKWPROGKGSYWTLOPDSYNMFENGS

FLRRRRRFKKKDUSKEKEBRAHLKEPPPAASKGAPATPHILADAPKEAEKKVVIKSEAA
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TLRTSPPGGELSPGAGRAGIVVPPLALPYAAAPPAYQGPCAGGLEAGAAGGYCCSMR
MANLYTGAERPAHMCVPPALDEALSDHPSGPTSPLSALNLAAGGEGALAATGHHHQHH
GHHHPQAPPPPPAQPQPTPQPGAAAAQAASMYLNHSGDLNHLPGHTPAAQQTFPN
REMFNSHRLGIENSTLGESQVSGNASCQLPYRSTPPLYRHAAPYSYDCTKY
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                                                                                                                                   Total Total (1998)
Miura, N.
Direct Submission
Submitted (18-SEP-1996) N. Miura, Akita University School of
Medicine, Department of Biochemistry, 1-1-1 Hondo, Akita 010,
Location/Qualifiers
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100.0%; Pred. No. 4.5e-169;
cive 0; Mismatches 0; Indels
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/product="Mesenchyme_Fork_Head-1"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
Mol_type="genomic DNA"
/db xref="taxon:9606"
1197. 2702
gene="WRH-1"
1197. .2702
/gene="WRH-1"
                                     (3), 489-492 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76765 AGCGGGGCCGGCCGCCTTGCCCCGGGGCGCCCTCCAGGATGCCGATCCGCCCGGTC 76706
                                                                                                                                                                                                                                                                                                                                                                                                        TCACCAAAATGTGATCATAAAATAAATTTTAATAAGATATAAACTTTTTAAAAAGTTTTCA 77185
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                                                                                                                                             CTGCCATTCCAATCCAGCGCGTTTGCTTTTGAATCCATTACACCTGGGCCCCCATAATTA
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                                                                                  Score 954; DB 9; Length 168656;
Pred. No. 4.7e-163;
0; Mismatches 5; Indels 2;
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-46309"
                                                                                    Query Match 96.8%;
Best Local Similarity 99.3%;
Matches 979; Conservative
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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                           ROD 27-NOV-2003
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all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats, all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. (Dases I to 178416)
Cordes, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-323K23
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA linear ROD 27-NOV-
from chromosome 8, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (06-AUG-2003) Genome Sequencing Center, 4444 Forest
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 178416)
Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequencing Center, 4444 Forest 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Sequencing Center, 4444 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://genome.wustl.edu.
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: M_BB0323K23
                                                                                                                                                        AC127554 178416 bp
Mus musculus BAC clone RP24-323K23
76525 GCCGGCGAGCCGTCTCGGAAGCAGCA 76500
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                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-JUL-2002)
Parkway, St. Louis, MO (
4 (bases 1 to 178416)
                                                                                                                                                                                                                                                                     GI:33457241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-JUL-2003)
Parkway, St. Louis, MO (5 (bases 1 to 178416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 178416)
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Submitted (17-JUL
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Direct Submission
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AC127554.4
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39272 TTTGCTCTGAACCCATTACAACTAGGCCCCGATAATTAAGAAATCTAATTCTGCCTCT 39331
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                                                                                         23 TIGCTITIGAATCCATTACACCIGGGCCCCCATAATTAGGAAATCTAATTAGGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           1423. .52857
note="CpG_island (%GC=66.5, o/e=0.72, #CpGs=121)"
3367. .53484
rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.3%; Score 298.6; DB 10; Length 178416; Best Local Similarity 64.7%; Pred. No. 4.9e-44; Matches 595; Conservative 0; Mismatches 269; Indels 55; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="B4"
11852, .61997
rpt_family="MER1_type"
2247, .62549
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67019. .67319
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67684. .67898
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3365. 33521
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/rpt family="Alu"
55213- 55240
55241 55364
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/rpt family="Alu"
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13394. .33521
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50513. .60709
/rpt_family="B;
50886. .61042
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                      SOURCE INFORMATION:
The RECI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                          NEICHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC124170.
                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="Alu"
973_ .4026
rpt_family="B4"
269_ .8820
noce="CpG island (%GC=69.2, o/e=0.78, #CpGs=269)"
6848. .16980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="B4"
25838 .26022
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27267 .27380
                                                                                                                                                                                  organism="Mus musculus"
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                                                                                                                                                  Location/Qualifiers
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4.20799
                                                                                                                                                                                                                                                                                1791. .1839
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3846. .3972
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8700. 28801
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30809. 300-
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rrpt family="Alu"
0987. 31062
rrt family="ID"
1157. 31294
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http://genome.wustl.edu
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Direct Submission
Submitted (18-SEP-1996) N. Miura, Akita University School of
Medicine, Department of Biochemistry, 1-1-1 Hondo, Akita 010, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PECYGAGMGRSYAPYHHOPAAPKDIVKPPYSYIALITWAIONAPEKKITLNGIYOFIM
DR PPFYRENKOGWONSIRHNLSLNECFVKVPRDDKKPGKGSYWTLDPDSYNMFENGSF
LRRRRRFKKKDVPKDKEERAHLKEPPSITAKGAPTGTPVADGPKEAEKKVVVKSEAAS
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/db_xref="G1:1869969"

/db_xref="GA5-QF0":061850"

/db_xref="SWISS-PROT:061850"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1145 TTTGCTCTGAACCCATTACAACTAGGCCCCGATAATTAAGAAATCTAATTATTCGCCTCT
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    protein
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  and
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'product="mesenchyme_fork head-1 protein"
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genes reveals conservation of their gene
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                      structures
Genomics 41 (3), 489-492 (1997)
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2070. .3554
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2070. .3554
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Miura, N.
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ORIGIN
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Best Local S:
Matches 597
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REFERENCE
AUTHORS
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  3932 TCATCCATTAATAATAATAAAAAAAAATCTCCAGGCTCTTTCCTACTTACAAGGTCTTG 39391
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                                        187
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Isolation of the mouse (MFH-1) and human (FKHL 14) mesenchyme fork
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Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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                                                                                                                                                                                      AATGTGATCATAAAATTTTAATAAGATATAACT--TTTTAAAAAGTTTTCAAGTGA
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                                      GGGAGAGATATTTACTCTATTAATCCATTCTATTTTATATTTCAAATTGA-----T
                                                                                                                TTTTTTTAACAGAAAAGTGGCTATCTTTTTTTTTTGGCATGTGGGCCCATTCACCAA
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mesenchyme fork head-1 protein; MFH-1 gene.
Mus musculus (house mouse)
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898 TCTCGCGCTCTCTCTCGCTCTCAGGCCCCCCTCGCTCCCCCGGGCCGCAGTCCGTGCGCGAG
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                               1211. 89708: contig of 89708 bp in length

1709 89808: gap of 100 bp

1809 112141: contig of 22333 bp in length

142 112241: gap of 100 bp

1242 135060: contig of 22819 bp in length

15160: gap of 100 bp

15161 159805: contig of 24645 bp in length.

Location/Qualifiers
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89809. ;12141
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| fragment_chain:1"
| 112242. ;135060
| note="assembly_fragment:00365.0"
| 135161. ;159808
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/organism="Danio rerio"

/organism="Danio rerio"

/oloxe="Daye="Genomia DNA"

/db_xref="texon:7955"

/clome="DKEY-4017"

/clome="Lib="DanioKey"

1. 89708

/note="assembly fragment:01665

fragment_chain:1"
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51.8%; Pred. No. 7.3e-06;
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WORKING DRAFT SEQUENCE, 4 unordered
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Submitted (23-SPE-2003) Wellcome Trust Sanger Institute, Hinxton, Submitted (23-SPE-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBD 0.18A, UK. E-mail enquiries:
Zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 24, 2003 this sequence version replaced gi:32959697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopietrygil; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                       1685 GCTCTCCGGACCCTAGCTCGCTGACGCTGCGGGCTGCAGTTCTCCTGGCGGGGCCCCGAG
                                                                                                                                                                                                                                AGCCTCCTGCGCCCCTCGCGCGCGCGCGGGGTCCACCTTGGTCCCCAGGCCGCGGGG
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                                                                                                      1625 TTGAAACTTTTCCCAATCCCTAAAAGGGACTTTGCTTCTTTTCCGGGCTCGGCGCA
                                                                                                                                                GCCGCT - CGGACCCCGGCGCGCGCTGACCTTCGCTGCCGATTCGCTGG-GGGCTTGGAG
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Consensus quality: 157884 bases at least Q40
Consensus quality: 158168 bases at least Q30
Consensus quality: 18816 bases at least Q30
Insert size: 189505; sum-of-contigs
Insert size: 164881; 0.9% error; agarose-fp
Coulity coverage: 10.03x in Q20 bases; sum-of-contigs Quality
coverage: 9.49x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX546449.3 GI:35209399
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
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AUTHORS
TITLE
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zish.help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 7, 2003 this sequence version replaced gi:37805598.
                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, etinopterygii, Neopterygii, Teleostel, Ostariophysi, Cypriniformes, Cyprinidae, Danio.

( Pases 1 to 172457)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator, 100% of reads
Consensus quality: 171280 bases at least Q40
Consensus quality: 171415 bases at least Q30
Consensus quality: 171619 bases at least Q20
Insert size: 172357; sum-of-contigs
Insert size: 177300; 4.4% error; agarose-fp
Quality coverage: 10.42x in Q20 bases; sum-of-contigs Quality
coverage: 10.2x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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fragment_chain:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-108M10"
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1. .110971
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clone_end:T7
vector_side:left"
                       Danio rerio (zebrafish)
Danio rerio
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PM2A12B 869 bp DNA linear STS 29-MAY-2003
Penicillium marneffei STS, clone pm2a12.b, sequence tagged site.
                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
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Danchin, A. and Pascal, G.
Direct Submission
Submitted (08-WAR-2002) Danchin A., HKU-Pasteur Research Centre,
Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong
Location/Qualifiers
                                                                                                                                                                                                                                                                                                         Yuen,K.Y., Pascal,G., Wong,S.S., Glaser,P., Woo,P.C., Kunst,F.,
Cai,J.J., Cheung,B.Y., Medique,C. and Danchin,A.
Exploring the Penicillium marneffei genome
Arch. Microbiol. 179 (5), 339-353 (2003)
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48.9%; Pred. No. 3.7e-05;
cive 0; Mismatches 226; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:37727"
/clone="pm2a12.b"
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nes 218; Conservative
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Homo sapiens chromosome 15 clone CTD-3026N10 map 15, LOW-PASS SEQUENCE SAMPLING.
                                                                                             627 YMSTGMYGMYSSYKSMSWTSKMSYMGKMTCTNYTSMKGSTRRSKMGRWSGMSRMYMRWWK 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 YC-GCSYCGSSKWKYMSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSMMYMGSCGCYTR 149
                                                                                                                                                                                                                                                                                                   601
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103 TGAAGACGGAGTCGCCGCGGGGGCGGGGGGGGGGGTCTTAGAGCCGACGGATTCCTGC 362
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 51753)
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                                                                                                                                                                                                                                                 CGGGAGGGGGCGTGGCCCGAGGAAAGTAAAACTCGCTTTCAGCAAGAAGACTTTTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 MRKKTKYSKRCYCWRYATCYWCCCYRKRGWYSRRSMMRTAGKWKMRSWSRWCRSYSWYKM
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                                                                                                                                                                                   567 KMRKRKYMRYMKWKCTWRRCMCYRWGYTMYTTSRSRMMYTGRYKARYTSKRYMWYKYRK
                                                                                                                                                                                                                           CITITICCCAATCCCTAAAAGGGACTTGGCCTCTTTTTCTGGGCTCAGCGGGGCAGCCGCT
                                                                                                                                                                                                                                                                                                   543 GGGACCCCGGCGCGCTGACCCTCGGGGCTGCCGATTC-GCTGGGGGCTTGGAGAGCCTCC
                                                                                                                                                                                                                                                                                                                                                                           TGCGCCCCTCCTCGCGCGGGCCGAGGGTCCACCTTGGTCCCCAGGCCGCGGCGCGTCTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     662 TGGGTCCGCGGCCGCCCGCCTGCCGCCTGCCGCCGGGTCCTGGAGCCAGCGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone CTD-3026N10
Unpublished
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Patent: WO 03000898-A 5263 03-JAN-2003;
Syngenta Participations AG (CH)
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kukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideee, Oryzeae, Oryza.
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/organism="Oryza sativa"
/mol type="unassigned DNA"
/db_xref="taxon:4530"
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19. Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barren, B., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Liudblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Macdonald, P., Major, J., Matthews, C., Murphy, T., Naylor, J., Ngwon, C., Micol, R., Mathews, C., Raga, V., Murphy, T., Naylor, J., Ngwon, C., Micol, R., Norbu, C., Norman, C. H., Phunkhang, P., Plerre, N., Raymond, C., Retta, R., Seeman, S., Seman, S., Schupca, Roman, S., Schupch, Roman, S., Schupch, Roman, S., Schupch, Roman, S., Schupch, S., Vola, W., S., Schupch, S., Young, G., Zainoun, J., Vola, R., Wilson, B., Wu, X., Myman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

L. Submitted (17-Jul-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 17, 2002 this sequence version replaced gi:21426260.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker:html
                          Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lachoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdanlad, P., Major, J., Marquis, N., Matchews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Meman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Neil, D., Peterson, K., Phunkhang, P., Plerre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Senge-Thomann, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, W., Travers, M., Talamas, J., Tasfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Manan, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Manan, D., Ye, W.J., Young, G., Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 51753)
   Goyette, M., Graham, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o: contig of 745 bp in length
o: gap of 100 bp
o: contig of 721 bp in length
o: gap of 100 bp
contig of 705 bp in length
gap of 100 bp
contig of 731 bp in length
gap of 100 bp
   Galagan, J., Gardyna, S., Ginde, S., Gord, S.,
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Center clone name: 3026_N_10
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COMMENT

HTG 30-MAR-2000 LOW-PASS

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Estren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B. Brown, A., Burkett, G., Compopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, N., Klein, J., Gardyna, S., Ginde, S., Dones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McDanal, M., McDawan, P., McGur, K., Marada, C., Mlenga, V., Morrow, J., Meldrim, J., Meneue, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Neil, D., O'Neil, D., Murphy, T., Naylor, J., Schauer, S., Severy, P., Spencer, B., Stanger-Thomann, N., Schauer, S., Severy, P., Spencer, B., Stanger-Thomann, N., Schauer, S., Severy, P., Spencer, B., Theodoco, J., Tirrell, A., Trayananian, A., Talalmas, J., Voung, G., Zalmoun, J., Zimmer, A. and Zody, M.

Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftb.peanome.waefington.edu/RM/RepeatMasker:html
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 75144)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 3, clone RP11-336E13

Unpublished
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* sequencing reads that have not been assembled into

* contiggs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

be preserved.
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Web site: http://www-seq.wi.mit.edu
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AC027483.1 GI:7342227
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2466:
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SEQUENCE SAMPLING
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KEYWORDS
SOURCE
ORGANISM
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AC027483/c
                                                                                                                                                DEFINITION
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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Pred. No. 0.00023;
0; Mismatches 310; Indels 0;
econtig of 722 bp in length contig of 722 bp in length gap of 100 bp contig of 714 bp in length contig of 687 bp in length gap of 100 bp contig of 717 bp in length gap of 100 bp contig of 717 bp in length gap of 100 bp contig of 717 bp in length contig of 717 bp in length contig of 717 bp in length gap of 100 bp contig of 737 bp in length gap of 100 bp in length gap of 100 bp in length contig of 745 bp in length gap of 100 bp
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of 699 bp in length
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contig of 751 bp in length
gap of 100 bp
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gap of 100 bp
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Pred. No. 0.00024;
0; Mismatches 187; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of 100 bp be contig of 754 bp in length gap of 100 bp be contig of 764 bp in length gap of 100 bp be in length gap of 100 bp contig of 766 bp in length gap of 100 bp be in length gap of 100 bp be in length gap of 100 bp in length
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idarity 50.7%;
Conservative 0
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Best Local Similarity
Matches 192; Conserv
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NISTFLRAATAAYPIFQMIERNTVNKASSKAGRTLPSVVDGHIQFRDVRFAYFSRALLGGAGAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11305 bp DNA linear PLN 23-DEC-2002 (japonica cultivar-group) mdr11 gene for MDR-like ABC
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Place Croix du Sud, 2/20, 1348,
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SEOSASLSRELSKYSRELSENTSMGGSFRERCDSVSRYGTVETHEOGHKSKPVSMKK
LYSMIRPDRFEGUSGTVSARVAGGMELFALGVTOALVSYYMGWETTKREVATAVLE
CCGAVLTVVPHALEHLSFGIMGERLTLRVRERMFAALLRNEIGWFDDTSHTSSMLSSR
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RQQIGLVNQEPALFATSIRENILYGKGDASMDEINHAAKLSEAITFINHLPDRYETÇV
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AJ53661. G1:27368850
MDR-like ABC transporter; mdr11 gene.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
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|mol_type="genomic DNA"
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|1. .1130s
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/produc="mmR-like ABC transporter"
/protein_id="CAD59583.1"
/db_xref="GI:27368851"
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/db_xref="SPTREMBL:Q8GU75"
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Submitted (27-NOV-2002) Ducos E.,
Unite de Biochimie Physiologique,
BELGIUM
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JOURNAL
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Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
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Cai,J.J., Cheung,E.Y., Medigue,C. and Danchin,A.
Exploring the Penicillium marneffel genome
Arch. Microbiol. 179 (5), 339-353 (2003)
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|clone="pm/f8.g"
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8.1%; Score 79.6; DB 11;
Best Local Similarity 50.7%; Pred. No. 0.00015;
Matches 229; Conservative 0; Mismatches 219;
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Penicillium marneffei STS, clone
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AL685189.1 GI:19336534
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Danchin, A. and Pascal, G.
Direct Submission
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VMVAHRLSTIKNADVISVLQDGKIIEQGAHHQLIENRNGAYHKLVSLQQQQQQQQQQ
                     LAMAPDIIKGNOMVSSVFEILDRKTDVLIDAGNDVKRVEGVIELRGVEFRYPARPEVV
KWFWKGYGGNLGKSYLKANMLAAEAVSNIRTVAAFCAEEKVIKLYADELKEPAKOSFR
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536. .711
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85434 bp DNA linear HTG 04-JUN-2000
HOMO sapiens chromosome 15 clone CTD-2242M2 map 15q15, LOW-PASS
SECURINE SAMPLING.
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2 (bases I to BS434)
2 (bases I to BS434)
2 (bases I to BS434)
2 (bases I, Option of human chromosome IS DISS146-DISS117 region Unpublished
2 (bases I, to BS434)
3 (bases I, Option of Dischoff, R., Pleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T.
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Submitted (25-APR-2000) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
ON Jun 4, 2000 this sequence version replaced gi:7644476.
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4066 cécedededececececececedecececececece 4007
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Web site: http://chroma.mbt.washington.edu/msg_www
Contact: learowen@systemsbiology.org
Contact: Summary Statisfics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator aig pye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
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Homo sapiens (human)
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Query Match

8.1%; Score 79.6; DB 8; Length 11305;
Best Local Similarity 55.4%; Pred. No. 0.00021;
Matches 211; Conservative 0; Mismatches 164; Indels 6;

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Gaps 9

30068 30167; gap of unknown length 30068 30092 310991; contig of 804 bp in length 31092 310901; gap of unknown length 31092 310901; gap of unknown length 31086 310901; gap of unknown length 31086 31086; gap of unknown length 31086 35355; contig of 811 bp in length 31086 310801; gap of unknown length 310801 310801; gap of unknown length 310801 310801; contig of 812 bp in length 310801; gap of unknown length 310801; contig of 812 bp in length 310801; contig of 812 bp in length 310801; contig of 800 bp in length 410801; gap of unknown length 410801; gap of unknown length 41091; gap of unknown length 51091; gap of unknow	5988: contig 5988: gap of 60985: contig 60895: gap of 61705: contig 61805: gap of 62606: gap of 62706: gap of 63517: contig 63517: gap of
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to completion. In the event that ted, the accession number will gap of unknown length contig of 138 bp in length gap of unknown length contig of 796 bp in length gap of unknown length contig of 796 bp in length gap of unknown length contig of 796 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 798 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 797 bp in length gap of unknown length contig of 797 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 799 bp in length gap of unknown length contig of 805 bp in length gap of unknown length contig of 805 bp in length gap of unknown length length contig of 805 bp in length gap of unknown length length gap of unknown length length contig of 808 bp in length gap of unknown length length	gap contigues of c
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Submitted (16-JAN-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Jan-16, 2003 this sequence version replaced gi:26665814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Mij; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 22817 bases at least Q40
Consensus quality: 223040 bases at least Q20
Insert size: 220000; agarose-fp
Insert size: 22504; sum-of-contigs
Quality coverage: 11.88 in Q20 bases; sum-of-contigs
                                                                                                                                  Center: Washington University Genome Sequencing Center
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                                                                                                                                                                                                                                                                                               -------- Summary Statistics
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/note="assembly_name:Contig16"
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/note="assembly_name:Contig18"
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/note="assembly_name:Contig17"
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22968. .33389
.note="assembly_name:Contig20"
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/note="assembly_name:Contig21"
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.07777. .224777
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mol type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP24-444115"
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ACI38109

Mus musculus chromosome UNK clone RP24-444115, WORKING DRAFT

SEQUENCE, 8 unordered pieces.

ION ACI38109.2

ACI38109.2

Mus musculus (house mouse)

ISM Mus musculus (house mouse)

ISM Wus musculus (house mouse)

ISM CE I (bases 1 to 224777)

ACI38100.2

L (bases 2 to 224777)

ACI38100.2

ACI3810.2

ACI38100.2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (13-DEC-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 224777) McPherson, J. D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.0%; Score 79.2; DB 2; Length 85434; Best Local Similarity 48.7%; Pred. No. 0.00032; Matches 219; Conservative 0; Mismatches 229; Indels 2;
        64420: contig of 803 bp in length 64520: gap of unknown length 65228: contig of 808 bp in length 65428: gap of unknown length 66234: contig of 806 bp in length 67118: contig of 784 bp in length 67218: gap of unknown length 67218: gap of unknown length 68008: contig of 796 bp in length 68008: contig of 793 bp in length 68001: contig of 793 bp in length
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McPherson, J.D. and Waterston, R.H.
Direct Submission
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Chases 1 to 93821)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldakin, J., Barna, N., Beckerly, R., Bedakin, J., Barna, N., Beckerly, R., Bedakin, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dowar, K., Domino, M., Doyle, M., Fenestor, J., Ferretra, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Rardia, A., Klein, J., Ianders, T., Chonson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, N., McEwan, E., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, V. Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Schery, P., Spencer, B., Stange-Thomann, N., Subramanian, A., Talamas, J., Wu, X., Wyman, D., Ye, W.J., Zhmer, A. and Zody, M.

Lirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zhmer, A. and Zody, M.

Lirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zhmer, A. and Zody, M.

Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 13, 2000 this sequence version replaced gi:6705503.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Homo sapiens clone RP11-165K4, LOW-PASS SEQUENCE SAMPLING.
AC021596
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 93821)
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                                                                                                                                   Gaps
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,
Length 224777;
      Score 79; DB 2; Length 224
Pred. No. 0.00038;
0; Mismatches 176; Indels
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B.08;
52.4%;
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Homo sapiens (human)
                                                                                                                                   Matches 197; Conservative
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      Query Match
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIGS
                                                                                                                                                                                                                                                                                                                                                           * sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                      Web site: http://www.seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Froject Information
Center project name: L5/87
Center clone name: 165_K-4
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Best Local Similarity 49.0
Matches 227; Conservative
                 63494
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ATORNEAL STATES ATTORNATION:

PILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TVPE: MUCLEIC acid
TVPE: MUCLEIC acid
TVPE: MUCLEIC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                US-08-758-306-137/c
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Sequence 1199, App
Sequence 1109, App
Sequence 5500, App
Sequence 5500, App
Sequence 5501, App
Sequence 2391, App
Sequence 2392, App
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35, Appl
10, Appl
85, Appl
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                                                                                                       March 25, 2004, 09:55:14 ; Search time 1.77026 Seconds (without alignments) 2821.370 Million cell updates/sec
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H, Appl
H, Appl
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/ggr2_6/ptodata/2/ina/5B_COMB.seq:*
/ggr2_6/ptodata/2/ina/6A_COMB.seq:*
/ggr2_6/ptodata/2/ina/RECOMB.seq:*
/ggr2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/ggr2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-758-306-139
US-08-758-306-11109
US-08-758-306-111109
US-08-758-306-111109
US-09-711-772B-2392
US-09-371-772B-2392
US-09-371-772B-2392
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US-09-780-175-137
US-09-780-175-138
US-09-781-681-19
US-08-175-138
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US-09-199-542B-85
US-09-198-177-114
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                                                                                                                                                                            US-09-963-285-1_COPY_223_231
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Maximum Match 100%
Listing first 45 summaries
                                                                      - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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Perfect
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No.
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54, Appl
17, Appl
635, App
1408, Ap
2684, Ap
3, Appli
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                                                              GEGUENCE 137, Application US/08758306
Fadeunce 137, Application US/08758306
Fadeunce 137, Application US/08758306
Fadeunce 137, Application US/08758306
FITLE OF INVENTION: METHOD AND REAGENT FOR THITLE OF INVENTION: TREATMENT OF DISEASES
FITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: GAWMA-CHAIN EXPRESSION
FITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
FITLE OF INVENTION
FITL
                                      58-287B-17
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FASISGA VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFTCATION: 514
PRIOR APPLICATION DATA:
FILING DATE: FILING DATE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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Length 17;
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| Sequence 1111/Application US/08758306
| Patent No. 5807743
| GENERAL INFORMATION:
| APPLICANT: Stinchcomb, Dan T. APPLICANT: Stinchcomb, Dan T. APPLICANT: MCSViggen, James A. TITLE OF INVENTION: METHOD AND REAGENT FOR THE TITLE OF INVENTION: MESCOLARED WITH TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR TITLE OF INVENTION: ASSOCIATED WITH TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION NUMBER OF SEQUENCES: 1379
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Lyon & Lyon | STREET: 633 West Fifth Street | STREET: 633 West Fifth Street |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 9; DB 1; L 100.0%; Pred. No. 2.8e+03;
                                n, James A.
METHOD AND REAGENT FOR THE
TREATMENT OF DISEASES
            APPLICAT: MCSW-SW METHOL TITLE OF INVENTION: METHOL TITLE OF INVENTION: METHOL TITLE OF INVENTION: ASSOCIATED MITH TITLE OF INVENTION: ASSOCIATED MITH TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION NUMBER OF SEQUENCES: 1379 CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES: Lyon & Lyon STREET: Suite 4700
STREET: Suite 4700
TREET: Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                     STREET: Suite 4700
STREET: California
COUNTRY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTEN READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTEN: IBM COMPATIALE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRASCATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION SATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERNENCE/OCKET NUMBER: 212
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (7.13) 955-0440
INFORMATION FOR SEQ ID NO: 1109:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: MCSWiggen, James A.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: ASSOCIATED WITH
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
NUMBER OF SEQUENCES: 1379
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
CHAPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Le
. 2.8e+03;
               Query Match 100.0%; Score 9; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
COMPUTER: 1EM Compatible
COMPUTER: 1EM Compatible
OPERATING SYSTEM: 1EM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION BATA:
FILING DATE: FILING DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TREECCOMMUTICATION INFORMATION:
TELECCOMMUTICATION INFORMATION:
TELECCOMMUTICATION INFORMATION:
TELECCOMMUTICATION INFORMATION:
TELECCOMMUTICATION INFORMATION:
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                                                                                                                                                                                                                                                                            Sequence 139, Application US/08758306
Patent No. 5807743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTY: U S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-758-306-139/c
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US-08-758-306-139
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Gaps

STREET: CITY: Lo

RESULT 3 US-08-758-306-1109/c ; Sequence 1109, Application US/08758306 ; Patent No. 5807743 ; GENERAL INFORMATION:

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Gaps
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Sequence 5501, Application US/08584040

Patent No. 6346398

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Barchoho, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaine
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESSE:
ADDRESSER: Lyon & Invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 9; DB 4; L 100.0%; Pred. No. 2.8e+03;
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CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: BEN COMPACHE, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: DBM COMPACHE, 1.04 Mb
MEDIUM TYPE: Storage
COMPUTER: DBM COMPACHE, 1.00 S.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WATCHING, RICHARD 1.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTONINEY/ASENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
RELERANTOLOCKET NUMBER: 218/064
TELEFRAM: (213) 499-1600
TELEFRAM: (213) 499-1600
TELEFRAM: (213) 955-0440
TELEFRAM: 67-3510
INFORMATION FOR SEQ ID NO: 5500: 5EQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IE: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5501:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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US-08-584-040-5500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5500, Application US/08584040

Patent No. 6346338
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: TREATMENT OF DISEASES OF
TITLE OF INVENTION: OF VACULAR ENDOTHELIAL
TITLE OF INVENTION: OF VACULAR ENDOTHELIAL
TITLE OF INVENTION: OF VACULAR ENDOTHELIAL
TITLE OF INVENTION: GROWHY FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
                                                                                                                                       COMPOTER: IBM Compatible
COMPOTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,306
FILING DATE: December 3, 1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                 ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,22/13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: 67-3510
INFORMATION FOR SEQ ID NO: 1111:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACAAATGTT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ACAAATGTT 3
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US-08-584-040-5500/c
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                             COUNTRY:
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Sequence 137, Application US/09780175
PATENT NO. 6440738
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Jacquelline Wyatte
TITLE OF INVENTION: ANTIESSEE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
FILE REFERENCE: RTS-0164
CURRENT APPLICATION NUMBER: US/09/780,175
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 154
EBNGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Robert McKay
APPLICANT: Susan M. Freier
APPLICANT: Jacqueline Wystr
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION
FILE REPERENCE: RTS-0164
CURRENT APPLICATION NUMBER: US/09/780,175
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 154
LENGTH: 20
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                                                                                                                                    Length 17;
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ilarity 100.0%; Pred. No. 2.8e+03;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 9; DB 4; L
100.0%; Pred. No. 2.8e+03;
                                                                                                                                    100.0%; Score 9; DB 4; I 100.0%; Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antisense Oligonucleotide US-09-780-175-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Antisense Oligonucleotide US-09-780-175-138
                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Patent No. 6440738
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                              Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
                   ; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-7728-2392
                                                                                                                                                                                                                                                                                                                                                                   US-09-780-175-137/c
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US-09-780-175-138/c
SEQ ID NO 2392
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APPLICANT: Barco, Pam
APPLICANT: Barco, Pam
APPLICANT: Stinchcomb, Dam
TITLE OF INVENTION: Levels of Vacuular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vacuular Endothelial Growth Factor Receptor
FILE REPRENCE: 1996-10 (237/198)
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: WIMBER: US/09/371,772B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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                                                                                                                                                          Length 17;
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                                                                                                                                                                                                      0; Indels
                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT B
US-09-371-772B-2392/c
; Sequence 2392, Application US/09371772B
; Patent No. 656127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc:
. APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-371-772B-2391/c
1 Sequence 2391, Application US/09371772B
2 Patent No. 6566127
3 GENERAL INFORMATION
3 APPLICANT: Ribozyme Pharmaceuticals, Inc.
3 APPLICANT: Ribozyme Pharmaceuticals, Inc.
3 APPLICANT: SinchComb, Dam
3 APPLICANT: StinchComb, Dam
3 APPLICANT: Escobedo, Jaime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 9; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                      LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                  1 ACAAATGTT 9
                                                                                                                                                                                                                                                                               11 ACAAATGTT 3
                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2391
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TOPOLOGY: ]
US-08-584-040-5501
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LENGTH: 17
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NESULT 13

UG-06-743-57B-240/C

UG-06-743-57B-240/C

Sequence 240, Application US/08743637B

Patent No. 5994064

GENERAL INFORMATION:

APPLICANT: PERGERON, Michel G.

APPLICANT: PERGERON, Michel G.

APPLICANT: PERGERON, Michel G.

APPLICANT: PERGERON, Machel G.

APPLICANT: PERGERON, Machel G.

APPLICANT: PERGERON, Machel G.

TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT

TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT

TITLE OF INVENTION: ANTIBLOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS

TITLE OF INVENTION: ANTIBLOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS

TITLE OF INVENTION: ANTIBLOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS

TITLE OF INVENTION: ANTIBLOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS

COMPUTES: ALI EAST WISCONSIN

COMPUTER: PLOUP OF GISK

COMPUTER: IBP PC COMPATION AND ANTIBLOTIC RESISTANCE COMPUTER: LBM PC COMPATION DATA:

APPLICATION NUMBER: US 08/526,840

FILING DATE: 11-SEP-1995

ATCHARAT MADELICATION NUMBER: 13,433

REFERENCE/DOCKET NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 35,433
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COMPUTER: REALBABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DIGANE C
REGISTRATION NUMBER: 34,941
REPERSENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTER
SEQUENCE CHARACTER
LENGTH: 22 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||||||
12 ACAAATGTT 20
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TOPOLOGY: 111
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                                                                  Sequence 19, Application US/08512681
; Sequence 19, Application US/08512681
; Patent No. 575596
; GENERAL INFORMATION:
    APPLICANT: Obefier, Peter J.
    APPLICANT: Underhill, Peter A.
    TITLE OF INVENTION: Detection of DNA Heteroduplex Molecules
    TITLE OF INVENTION: Detection of DNA Heteroduplex Molecules
    TITLE OF INVENTION: Detection of DNA Heteroduplex Molecules
    TITLE OF INVENTION: Methods for Comparative Sequencing
    NUMBER OF SEQUENCES: 29
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Dehlinger & Associates
    STREET: 350 Cambridge Ave., Suite 250
    CITY, Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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APPLICANT: MEZES, PETER S
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: ANDERSON, WH KERR
APPLICANT: SCHOLOM, JEFFREY
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P.O. BOX 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 9; DB 1; Length 22; 100.0%; Pred. No. 2.8e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:

ZIP: 94306

COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TEADALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Datentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,681
FILING DATE:
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: EVANA SUBART: 38,443
REFERENCE/DOCKET NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 8600-0155
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHRRACTERISTICS:
IENGTH: 22 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE: DYS234 REVERSE PRIMER US-08-512-681-19
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Patent No. 5993813
GENERAL INFORMATION
APPLICANT: GOURLIE, BRIAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIDLAND
                                                               US-08-512-681-19/c
                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Pal
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  822-028-35
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100.0%; Score 9; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                               Query Match
100.0%; Score 9; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,285

FLING DATE: 07-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/040687

FILING DATE: 13-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: ULER: DOATE: 31-MAR-1993

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-37,075C

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARCERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compacible
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35, Application US/08479285 Patent No. 6207815
                     TELEPHONE: (414) 277-5000
TELEFAX: (414)277-5591
INPORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TELECOMMUNICATION INFORMATION: TELEPHONE: (414) 277-5000
                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P.O. BOX 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                           1 ACAAATGTT 9
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JS-08-479-285-35
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1 ACAAATGTT 9

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APPLICANT: Mezee, Peter S
APPLICANT: Gourlie, Brian B
APPLICANT: Gourlie, Brian B
APPLICANT: Gourlie, Brian B
APPLICANT: Rixon, Mark W
APPLICANT: Applan, Donald A
APPLICANT: Schlom, Jeffrey
ITLE OF INVENTION: Poboing Method for Identifying Antibodies
ITLE REFERENCE: 37075H-CIPI
CURRENT FILING DATE: 2000-02-14
FRICA PLING DATE: 1993-03-31
PRIOR FILING DATE: 1993-03-31
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1988-10-24
PRIOR FILING DATE: 1988-10-24
PRIOR FILING DATE: 1988-10-19
PRIOR FILING DATE: 1988-10-24
PRIOR FILING DATE: 1988-10-19
SPRIOR FILING DATE: 1988-10-24
PRIOR FILING DATE: 1988-10-30
NUMBER OF SEQ ID NOS: 74
SOFTWARE: MICROSOFT WOR' 97 SR-2
LENGTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:

NAME/KEY: misc_feature

LOCATION: 1...27

COTHER INFORMATION: Oligo CC83 L intron(-)

US-09-503-653A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 25, 2004, 15:34:20 Job time : 2.77026 secs
RESULT 15
US-09-503-653A-35
'Sequence 35, Application US/09503653A
"=+ant No. 6641999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ACANATGIT 20
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Best Local Similarity
Matches 9; Conserv
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March 25, 2004, 10:03:04; Search time 14.7262 Seconds (without alignments) 4297.861 Million cell updates/sec
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1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*

3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/prodata/1/pubpna/DS06_PUBCOMB.seq:*

6: /cgn2_6/prodata/1/pubpna/DS08_NEW_PUB.seq:*

7: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*

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7: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*

7: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*

7: /cgn2_6/prodata/1/pubpna/US108_PUBCOMB.seq:*

7: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2458946 seqs, 1861504846 residues
                                                                                                                                                                                                                                                                                                                        US-09-963-285-1_COPY_359_375
17
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                     OM nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 9718, Ap	Sequence 1, Appli	Sequence 107702,	Sequence 82796, A	Sequence 10003, A	Sequence 977, App	Sequence 1138, Ap	Sequence 64036, A	Seguence 17187, A	Sequence 22032, A	Sequence 242033,	Sequence 242034,	Sequence 141232,	Sequence 63676, A	Segmence 148185.
SUMMARIES	QI	US-10-027-632-9718	US-09-963-285-1	US-10-424-599-107702	US-10-424-599-82796	US-09-764-891-10003	US-10-205-428-977	US-10-131-827-1138	US-10-424-599-64036	US-09-814-353-17187	US-10-424-599-22032	US-10-027-632-242033	US-10-027-632-242034	US-10-424-599-141232	US-10-424-599-63676	US-10-027-632-148185
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	Query Match Length DB	962	6458	493	2523	21619	21619	50	359	386	493	589	589	909	616	676
de	Query Match	100.0	100.0	94.1	94.1	94.1	94.1	90.6	90.6	90.6	90.6	90.6	90.6	90.6	90.6	9.06
	Score	17	17	16	16	16	16	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4
	Result No.		7	m	4	Ŋ	φ υ	7	60	g,	10	c 11	c 12	13	c 14	ני

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Gaps

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Query Match 100.0%; Score 17; DB 15; Length 962; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 17; Conservative 0; Mismatches 0; Indels (

1. TGTGGAAGGAATAATA 17

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Sequence 37752, A Sequence 43641, A Sequence 256263, Sequence 256264, Sequence 256264, Sequence 24, Appl Sequence 12, Appl Sequence 17, Appl Sequence 27, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 31, Appl Sequence 68, Appl Sequence 13766, A Sequence 13766, A Sequence 1366, A Sequence 1367, Appl Sequence 1366, Appl Sequence 1366, Appl Sequence 1367, Appl Sequence 1	Sequence 1367, Ap Sequence 1368, Ap Sequence 1368, Ap Sequence 1368, Ap Sequence 1369, Ap Sequence 1, Appli Sequence 234237,	Single Nucleotide
12 US-10-424-599-37752 15 US-10-424-599-43641 15 US-10-627-632-256262 15 US-10-027-632-256263 14 US-10-027-632-256264 15 US-10-027-632-256264 16 US-10-087-080-24 17 US-10-274-17-12 18 US-10-274-17-12 19 US-10-341-434-17 15 US-10-341-434-17 15 US-10-087-080-27 16 US-10-221-613-351 17 US-10-221-613-351 18 US-10-221-613-351 19 US-09-764-085-68 10 US-09-764-085-68 10 US-09-764-085-68 10 US-09-764-085-68		24,10027632 And Loation and Mapping of Ephisms in the Human Ge of 218,006 12 60/218,006 25 60/198,676 5 60/198,676 5 60/198,218 5 60/195,218 5 60/166,358 5 60/166,358 5 60/166,002 9 9 Version 4.0
	.6 16285 .6 16285 .6 16285 .6 16285 .6 16285 .6 16285 .6 16285 .6 180557 .6 180557 .6 186510 .2 2 2 6 2 16	20,000,000,000,000,000,000,000,000,000,
	444444444444000 0000000000000000000000	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		REGULT 1 OS-10-027-532 CBOURAL INFO APPLICANT: TITLE OF IN PRIOR FILIN

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Sequence 82796, Application US/10424599
| Publication No. US20040031072A1
| Publication No. US20040031072A1
| Publication No. US20040031072A1
| APPLICANT: La Rosa Thomas J
| APPLICANT: Cao Yongwei
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| FILE REPERENCE: 38-21(53223)B | CURRENT APPLICATION NUMBER: US/10/424,599 | CURRENT PILING DATE: 2003-04-28 | NUMBER OF SEQ ID NOS: 285684 | SEQ ID NOS: 285684
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100.0%; Pred. No. 6.5e+02;
.ive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 10031 LENGTH: 21619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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Sequence 917, Application US/10205428
Publication No. US20030108907A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.1%; Score 16; DB 12; I
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_45782C.1
US-10-424-599-82796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 10003, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5310 rGrGGAAGGAArAAr 5295
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                                             233 GTGGAAGGAATAATA 248
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Best Local Similarity 100.0
Matches 16; Conservative
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CRGANISM: Homo sapiens
US-09-764-891-10003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-09-764-891-10003/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
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; Sequence 10702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: Exeratic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass;
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5323) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-4-28
; NUMBER OF SEQ ID NOS: 285684
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100.0%; Score 17; DB 9; Length 6458;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
94.1%; Score 16; DB 12; Length 493;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(493)
OTHER INFORMATION: unsure at all n locations
FEATURE:
                                                                                                           US-09-90-128-128-1
Sequence 1, Application US/09963285
Patent No. US2002009707A1
GENERAL INFORMATION:
APPLICANT: Enexbck, Sven
APPLICANT: Krock, Katarina
APPLICANT: Krock, Katarina
APPLICANT: Krodk, Lena
APPLICANT: Wasserman, Wyeth
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFRENCE: 13425-04201
CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-05-06
PRIOR PLING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 rerechaecharann 375
727 TGTGGAAGGAATAAATA 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (2235)...(3737)
US-09-963-285-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-10-424-599-107702
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
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APPLICANT: Can Vinua I
APPLICANT: Can Vinua I
APPLICANT: Can Vinua I
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBING: 38-21(5323)8
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 64036
LENGTH: 359
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APPLICANT: Include, dames

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: DEBNITIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

FILE REFERENCE: MRI-006B

CURRENT APPLICATION NUMBER: US/09/814,353

CURRENT FILING DATE: 2001-03-21

PRIOR PELICATION NUMBER: US 60/191,031

PRIOR PELICATION NUMBER: US 60/207,124

PRIOR PELICATION NUMBER: US 60/207,124

PRIOR PELICATION NUMBER: US 60/207,124

PRIOR PELICATION NUMBER: US 60/211,940

PRIOR PELICATION NUMBER: US 60/211,940

PRIOR PELICATION NUMBER: US 60/216,820

PRIOR PELICATION NUMBER: US 60/216,820

PRIOR PELICATION NUMBER: US 60/220,661

PRIOR PELICATION NUMBER: US 60/220,661

PRIOR PELICATION NUMBER: US 60/220,661

PRIOR PELICATION NUMBER: US 60/257,672

PRIOR PELICATION NUMBER: US 60/257,673

PRIOR PELICATION NUMBER: US 60/257,673
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Pred. No. 8.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_28838C.1
MS-10-424-599-64036
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                                                                                                                                                                  Sequence 64036, Application US/10424599
Publication No. US20040031072A1
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              27 TGTGGAAGGAATAAAA
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Best Local Similarity 94.1
Matches 16, Conservative
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ORGANISM: Glycine max
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US-10-131-827-1138

US-10-131-827-1138

Sequence 1139, Application US/10131827

PUBLication No. US20040009479A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Woodward, Robert

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES

TITLE OF INVENTION: UNMBER: US/10/131,827

CURRENT FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-22

PRIOR FILING DATE: 2001-10-06

NUMBER OF SEQ ID NOS: 9090

SOOFWARE: Patentin Version 3.1

SEQ ID NO 1138

LENGTH: 50
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Pred. No. 6.5e+02;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/205,428
CURRENT FILING DATE: 2002-07-26
PRIOR PEDLICATION NUMBER: 09/764,892
PRIOR PELLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PELLING DATE: 2000-01-31
PRIOR PELLING DATE: 2000-01-31
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-06-28
PRIOR PELLING DATE: 2000-06-28
PRIOR PELLING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR PELLING DATE: 2000-07-11
PRIOR PELLING DATE: 2000-07-11
PRIOR PELLING DATE: 2000-07-11
PRIOR PELLING DATE: 2000-07-14
PRIOR PELLING DATE: 2000-07-14
PRIOR PELLING DATE: 2000-07-17
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Best Local Similarity 94.1%;
Matches 16; Conservative
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US-10-131-827-1138
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CONGANISM: Homo sapiens
US-10-205-428-977
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LENGTH: 21619
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Sequence 14132. Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Gas Thomas J
APPLICANT: Kovalic David K
APPLICANT: Anow Yinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                     Length 589;
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                  Query Match 90.6%; Score 15.4; DB 15; Best Local Similarity 94.1%; Pred. No. 8.5e+02; Matches 16; Conservative 0; Mismatches 1;
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Pred. No. 8.5e+02;
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OTHER INFORMATION: Clone ID: PAT_MRT3847_98544C.1
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90.6%; Score 15.4; D

Best Local Similarity 94.1%; Pred. No. 8.5e

Matches 16; Conservative 0; Mismatches
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Publication No. US20030204075A9
GENERAL INFORMATION:
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US-10-027-632-242034/c
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US-10-027-632-242034
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                                                                                                                                                                                                     APPLICANT: La Novalionas J
APPLICANT: Low Avoid to David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEQ ID NOS: 285684
SEQ ID NO 22032
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GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/02.04-30

PRIOR APPLICATION NUMBER: US 60/138,606

PRIOR PILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-29

PRIOR FILING DATE: 2000-07-29

PRIOR APPLICATION NUMBER: US 60/198,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-109-28

PRIOR FILING DATE: 1999-109-28

PRIOR FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FASISEO for Windows Version 4.0

LENGTH: 589
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US-10-424-599-22032
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OTHER INFORMATION: unsure at all n locations
FEATURE:
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                                                                                                                                                 ; Sequence 22032, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                     348 rcredaaddaaraara 364
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ORGANISM: Glycine max
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US-10-027-632-242033/c
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GRGANISM: Human
US-10-027-632-242033
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US-10-424-599-22032
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Gaps

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Score 15.4; DB 15; Length 676;
Pred. No. 8.6e+02;
0; Mismatches 1; Indels 0:
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                                                                      Query Match

Best Local Similarity 94.1%; Pre
Matches 16; Conservative 0;
                                                                                                                                                                                                                                   233 TGTGGAATGAATAATA 217
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; ORGANISM: Human
US-10-027-632-148185
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US-10-424-599-63676/c

US-10-424-599-63676/c

Sequence 63676, Application US/10424599

Publication No. US20040031072A1

Sequence 63676, Application US/10424599

Publication No. US20040031072A1

Sequence 63676, Application US/10424599

Sequence 63676, Application No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 63676

LENGTH: 616
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR PAPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PELING DATE: 2000-07-12

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-113,83

PRIOR FILING DATE: 1999-113,83

PRIOR FILING DATE: 1999-113,83

PRIOR FILING DATE: 1999-10-8

PRIOR FILING DATE: 1999-10-8

PRIOR FILING DATE: 1999-09-28

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                                               90.6%; Score 15.4; DB 12; Length 606; 94.1%; Pred. No. 8.5e+02; ive 0; Mismatches 1; Indels 0
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US-10-424-599-63676
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SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 148185
LENGTH: 676
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US-10-027-632-148185/c
; Sequence 148185, Application US/10027632
; Publication No. US20030204075A9
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                                                                                                     Conservative
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Best Local Similarity
Matches 16; Conserve
                                               Query Match
Best Local Similarity
Matches 16; Conserv
US-10-424-599-141232
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Abg31996 Oligonucl Abg11997 Oligonucl Abg11997 Oligonucl Abg11997 Oligonucl Ada1999 Oligonucl Ada2592 Human WNT Abg25497 Oligonucl Abg25497 Oligonucl Abg25497 Oligonucl Adg8792 Human gen Adg1255 Oligonucl Adg1255 Oligonucl Abg1255 Oligonucl Adg1255 Oligonucl Adg1255 Oligonucl Adg26554 Human STA Add2654 Human GPC Ada26554 Human GPC Ada26554 Human GPC Add26554 Human GPC Add60227 Human GPC Add60221 Human GPC Add60221 Human GPC Add60221 Human GPC Add60221 Human GPC

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Run on:

Sequence:

Searched:

Database

Result

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New construct comprising a human FOXC2 gene, useful in gene therapy for treating obesity- or malnutrition-related diseases (e.g. obesity or hyperlipidemia), as well as for identifying compounds useful in treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOXC2; human, winged helix protein; FKHL14; transcription factor; forkhead gene; energy balance; adipose tissue; transgenic animal; obesity; malnutrition; hyperlipidaemia; diabetes; hypertension; annidiabetic; anorectic; hypolipaemic; hypotensive; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human winged helix protein FOXC2 cDNA.
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                                                                 ABQ31997
ABQ31994
ADA02552
ADB72290
ABQ52497
ABQ52496
AAK82792
AAK82792
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ABQ19255
ABQ19254
ADC86736
ADA02654
ADB72392
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1197. ,2705
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26-MAY-2000; 2000SE-00001982.
06-UIN-2000; 2000SS-00587945.
14-DEC-2000; 2000SE-00004629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-2001; 2001WO-SE000339
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The present sequence is that of cDNA was isolated from a human fat cell cDNA protein (see AAB82651). The CDNA was isolated from a human fat cell cDNA library using a mix of cDNA probes corresponding to DNA-binding domains from different winged helix proteins. FOXC2 (also designated FKHI14) was cone of the genes identified. Northern blotting showed FOXC2 to be expressed exclusively in human adult adipose tissue. A major role for CC FOXC2 in regulating energy balance and adiposity was demonstrated. The invention provides transgenic non-human mammals that are capable of expressing the human FOXC2 gene in their adipose tissue. Methods are corresponded for identifying compounds useful for the treatment of medical conditions related to obesity, such as obesity, non-insulin dependent diabetes, hypertension and hyperlipidemia (claimed). Such compounds are stimulate the biological activity of a human FOXC2 polypeptide. Methods are stimulate the biological activity of a human FOXC2 polypeptide. Methods are also provided for identifying compounds useful for the treatment of medical conditions related to malnutrition, such as anorexia (claimed). Such compounds decrease human FOXC2 gene expression or FOXC2 protein contivity. Gene therapy may be used as a method of treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 986; DB 4; Lengtn 52.
Pred, No. 1,6e-202;
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Best Local Similarity 100.0%;
Matches 986; Conservative 0
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216. .475
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/note= "Fragment of the FOXC2
claimed in claim 12"
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/note= "Fragment of the
claimed in claim 13"
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                                                                                                                                                /*tag= 1
/note= "Fragment of the FOXC2 promoter. Specifically
claimed in claim 1"
claimed in claim 1"
flate. .4629
/*tag= n
/note= "First exon according to the published form of
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'note= "Portion of polypeptide used in alternative
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100.0%; Score 986; DB 6;
Best Local Similarity 100.0%; Pred. No. 2e-202;
Matches 986; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "FOXC2"
/note= "Transcription factor"
2448. .2735
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1250. .1749
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P-PSDB; AAU79816.
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10-OCT-2000;
09-NOV-2000;
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                                                                               Transcription factor; FOXC2; antidiabetic; anorectic; antilipaemic; cardiovascular; FOXC2 polypeptide expression modulator; FOXC2 promoter; diabetes mellitus; obesity; hypercholesterolaemia; dyslipidaemia; cardiovascular disease; mouse medenchyme forkhead 1; MHF 1; gene; ds.
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Genomic DNA encoding mouse mesenchyme forkhead-1 (MHF-1)/FOXC2.
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/product= "MHF-1 or FOXC2"
/note= "Mouse mesenchyme forkhead 1"
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Pred. No. 1.4e-52;
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                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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10-OCT-2000; 2000US-0238897P.
09-NOV-2000; 2000SE-00004102.
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Best Local Similarity 64.9%;
Matches 597; Conservative
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P-PSDB; AAU79818.
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                                                                                                                                                                                                                                                                                                          Mus musculus
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The present invention relates to a method of identifying RNA-binding molecule comprising predicting the structure of RNA-fragment, selecting suitable predicted RNA fragment with an individual stem, synthesising a DNA-fragment corresponding to the RNA fragment, inserting the DNA fragment in upstream proximity of reporter assay gene to form reporter construct and performing a reporter gene assay which detects interaction between a molecule to be tested for RNA-binding and RNA fragment of the reporter construct. The method is useful for identifying an RNA binding molecule. The present sequence is human FOXC2 RNA fragment. This sequence
Identifying RNA-binding molecule by predicting structure of RNA fragment, synthesizing DNA fragment corresponding to predicted RNA structure, performing reporter gene assay after placing the DNA upstream of reporter
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1.6e-17;
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83.2%; Pred. No. 1
                                                                                                                                                                                                           29; 35pp; English
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Gaps

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bacterial infection; fungal infection; viral infection; rice;
                                                                                                  (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                22-JUN-2001; 2001WO-IB001105
                                                                                          22-JUN-2001; 2001WO-IB001105
                                                               WO2003000898-A1
                                                      Oryza sativa
                                                                        03-JAN-2003
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Hou Y; T, Zou

SA, Zhu

Goff

J, G Xie

Glazebrook Whitham S,

ֹא מׁ Cooper 3, Tao

Chen W, Co

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Chang H, Katagiri

WPI; 2003-175290/17.

Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant

Claim 27; SEQ ID NO 5263; 899pp; English

expression

gene

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4
           The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGMRWKRYKOKRAYWWRWWRCWKAGWARWMKSRYRWKWKKKYATRYYWKMAMTWWWSWRR
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                                                                                                                                                                                                                                                                                                                                     6 ATTCCAATCCAGCGCGTTTGCTTTTGAATCCATTACACCTGGGCCCCCATAATTAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGGTCTTTGGGAGAGATATTTTACTCTATTAATCCATTCTATTTATATTTCAAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543 CGGACCCCGGCGCGCTGACCCTCGGGGCTGCCGATTC-GCTGGGGGCTTGGAGAGCCTCC
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                                                                                                                                                                                                                                                           Length 2000;
                                                                                                                                                                                                                      Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                 412;
                                                                                                                                                                                                                                                       Query Match

8.1%; Score 79.8; DB 7;

Best Local Similarity 10.0%; Pred. No. 1.9e-07;

Matches 98; Conservative 460; Mismatches 412;
                                                                                                                                                                                illustrate the invention.
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The present invention relates to a method of identifying RNA-binding molecule comprising predicting the structure of RNA-fragment, selecting suitable predicted RNA fragment with an individual stem, synthesising a DNA-fragment corresponding to the RNA fragment, inserting the DNA fragment in upstream proximity of reporter assay gene to form reporter construct and performing a reporter gene assay which detects interaction between a molecule to be tested for RNA-binding and RNA fragment of the reporter construct. The method is useful for identifying an RNA binding molecule. The present sequence is human FOXC2 RNA fragment. This sequence is used to illustrate the method of the invention
                                                           961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying RNA-binding molecule by predicting structure of RNA fragment, synthesizing DNA fragment corresponding to predicted RNA structure, performing reporter gene assay after placing the DNA upstream of reporter
                             83
                                                                           GWKWRSKYSMCCKKYCSCCTKYCSYTGYYRYCKWYKYSYYKCYYCYCYWYMSYMRYKC
GCGCTCTCTCCCCTCTCAGGGCCCCCCTCCCCCCGGCCGCAGTCCGTGCGCGAGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 7; Lengtu ...

Pred. No. 8.4e-07;

Or ...

O; Indels
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                                                                                                                                                                                                                                                                                                                                                       Human; RNA binding molecule; FOXC2; ss.
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                                                                                                                      962 CCGGCGAGCCGTCTCGG 978
                                                                                                                                         SKKCTKRKYYYCYWSSG 12
                                                                                                                                                                                                                              AAD48768 standard; RNA; 75 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-2002; 2002WO-SE000677
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                                                                                                                                                                                                                                                                                                                        Human FOXC2 RNA fragment #2.
                                                                                                                                                                                                                                                                                          (first entry)
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Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasconstration; inflammation, allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; persentic ancer; hepatic metastasis;

prostate cancer; ss

409913886-A1

Synthetic.

Human adenosine Al receptor antisense oligonucleotide fragment.

(first entry)

05-JUL-1999

AAX53491;

AAX53491 standard; DNA; 114955

RESULT 7 AAX53491

61 GCGCGAGGGCGCCGG 75

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The specification describes antisense oligonucleotides (AAX52869-X55271).

directed against at least 2 mRNAs selected from target genes, coding and concoding regions of RNAs corresponding to target genes, gene initiation codins, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense cligonucleotides may be derived from sequences AAX55270-74. These multiple target oligonucleotides generated and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, including lung diseases, pulmonary vasoconstriction, impeded respiration, respiratory distances syndrome, pain, cystic fibrosis, pulmonary hypertension, cute asthma, allergies, asthma, impeded respiration, respiratory disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, melanoma, hepatic metastasses, as well as all types of cancers and prostate cancer.

Le the lungs, including breast and prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 37; 120pp; English.
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98US-00093972.
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891 CTGGCTCTCTCGCGCTCTCTCGCTCTCAGGGCCCCCCTCGCTCCCCCGGGCGCAGTCCGT

; Pred. No. 8.4e 13; Mismatches

62; Conservative

Query Match Best Local Similarity

Best Loca Matches

7.6%;

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Gaps

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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                       721 AGCGGGCCGGCGCTGCGCTTGCCCGGGGGGGCGCCTCCAGGATGCCGATCCGCCCGGTC 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 CTCGGACCCCGGCGCGCTGACCCTCGGGGCTGCCGATTCGCTGGGGGCTTGGAGAGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, cytosine methylation, 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide for detecting cytosine methylation SEQ ID NO 5817.
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                                                                                                                                 Sequence 1117 BP; 143 A; 72 C; 471 G; 123 T; 0 U; 308 Other;
                                                                                                                                                                                        0; Mismatches 279; Indels
                                                                                                                                                            Score 73; DB 9;
Pred. No. 4.8e-06;
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                                                                                                                                                               7.4%;
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ABQ19226/c
ID ABQ19226 standard; DNA; 687
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Matches 157; Conservative
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<u> GGGACTTGGCCTCTTTTTCTGGGCTCAGCGGGGAGCCGCTCGGACCCCGGCGCGCTGAC</u>
                                                                                                                                                                                                                  104962 SNINDINICEGGCEGGGGGGGGGGCGCGGCGGGCCGSNINDINEGGCCEGGGCGCCGC
                                                    CCTCGGGGGCTGCCGATTCGCTGGGGGCTTGGAGAGCCTCCTGCGCCCCCTCCTCCTCGCGCGGG
                                                                                                                                                              922 CCCCCCTCGCTCCCCCGGGCCGCAGTCCGTGCGGAGGGCGCCGGCGGCGAGCCGTCTCGGAAG
                                                                                                        CCGAGGGTCCACCTTGGTCCCCAGGCCGCGGGGGTCTCCGGGTCCGGGCCGCCGCCGC
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CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GPCR gene SEQ ID NO:1141.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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P-PSDB; ADC86689.
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ADC86688 standard;
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and candiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously, ABQ13410-ABQ5412 represent genomic DNA sequences used to illustrate the method for disclosure of the invention
                                                                                                                                                                                 Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
                                                                                                                                                                                                                                                                           Claim 12; 56pp + Sequence Listing; 56pp; German.
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  05-SEP-2000; 2000DE-01044543.
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from chemically treated DNA.
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                                            (EPIG-) EPIGENOMICS AG
                                                                                          Piepenbrock
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Sequence 687 BP; 11 A; 123 C; 446 G; 88 T; 0 U; 19 Other;

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7.1%; Score 70; DB 6; Length 687;
48.7%; Pred. No. 1.9e-05;
tive 0; Mismatches 184; Indels
             Local Similarity 48.7 es 175, Conservative
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ABQ19227 standard; DNA; 687

(first entry)

12-JUL-2002

ABQ19227;

RESULT 10
ABQ19227
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AC ABQ193
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DT 12-JUI

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-0pG-3', present in a genomic sample of DNA. The sample is treated chemically to convert ognomic sample of DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (BNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognesis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation of cell or cardiovascular canders of the certain of cell or cardiovascular canders of the central investigating cell differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation of cells of the cell of the cardior of cells of the cell of the cardior of cells of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell of the cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      717 GAGGAGCGGGCGCGCTGCGCTTGCCCGGGGCGCCCTCCAGGATGCCGATCCGCCC
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                      Oligonucleotide for detecting cytosine methylation SEQ ID NO 5818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 7.1%; Score 70; DB 6; I Local Similarity 48.7%; Pred. No. 1.9e-05; les 175; Conservative 0; Mismatches 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                             01-SEP-2000; 2000DE-01043826.
05-SEP-2000; 2000DE-01044543.
                                                                                                                                                                                                                                                                                                                                                                         01-SEP-2001; 2001WO-EP010074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for determining the degree of disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-371829/40.
                                                                                                                                                                                                                                                                WO200218632-A2.
                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                      07-MAR-2002
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Matches
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The specification describes antisense oligonucleotides (AAX52869-X55271)
directed against at least 2 mRAAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, coding and
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
end and the juxta-section between coding and non-coding regions and all
segments of RNAs encoding proteins associated with one or more diseases,
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX55272-74. These multiple target oligonucleotides
coditions or mixtures. Typical diseases and conditions are those
specifically AAX5180-271) can be used for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
acute asthma, allergies, asthma, impeded respiration, respiratory
distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, breast cancer, lung cancer, melanoma, hepatic metastasses, as
well as all types of cancer which may metastasize or have metastasized
to the lungs, including breast and prostate cancer
CCGGAGGCTGCCAGGAGCCGGGGCGCCCTCCCGCTCCCCTCCTCCCCCTCTGGCT 896
                                                                 canacicecececececececes de accesa de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constante de constan
                                                                                                                                                                                                               pulmonary hypertension; pulmonary vasoconstriction; emphysema; carcinoma; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; elanoma; hepatic metastasis;
                                                                                                                                              CTCTCGCGCTCTCTCTCTCTCAGGGCCCCCCTCGCTCCCCCGGGCCGCAGTCCGTGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adenosine Al receptor antisense oligonucleotide fragment
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                                                                                                                                                                                                                                                                                                                                                                                                 AAX53491 standard, DNA; 114955
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98US-00093972.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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09-JUN-1998;
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                                                                         414
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105601 CGGGCCGCGGGGCCGAGCCAGGGCCCNNHNNSCCGGGCCGGGCGGGCAGCCGGGCCG 105542
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                                                                                                      523 GGCTCAGCGGGGAGCCGCTCGGACCCCGGCGCGCTGACCCTCGGGGCTGCCGATTCGCT 582
           Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 0 U; 21427 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the
                                                                                                                                                                                                                                                   105541 CGGGGCCGAGGGCCCNNHNNNSVGCGGAGGCCGCCCNNHNNNSCGGCCCGCC
                                                                                                                                                                                                                              763 ATGCCGATCCGCCCGGTCCGCTGAAAGCGCGCGCCCTGCTCGGCCCGAGCGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                 823 GGGGCACCTCGCCCCGGAGGCTGCCAGGAGACCGGGGCCGCCCTCCCGGCTCCCCTCCT
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guanosine triphosphate-binding protein coupled receptor; gene therapy,
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                                            Length 114955;
                                        7.0%; Score 69.4; DB 2; 1
ilarity 37.0%; Pred. No. 0.0001;
Conservative 25; Mismatches 258;
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(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                          Similarity
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                                                            Best Local Simi
Matches 166;
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                                             Query Match
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CHIRON CORP.
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Matches
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                                                                      The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGGAGGCTGCCAGGAGACCGGGCCGCCCCTCCCGCTCCCCTCCTCCCCTCTGGCT 896
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                                                                                                                                                                                                                                                                                                                                                                                                 GAGGAGCGGGGCCGGCGCTGCGCTTGCCCGGGGCGCGCCCTCCAGGATGCCGATCCGCCC
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                            Sequence 3163 BP; 340 A; 345 C; 1360 G; 610 T; 0 U; 508 Other;
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detection; cancerous state; metastasis; identification; bro
oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                         0; Mismatches 191; Indels
guanosine triphosphate-binding protein coupled receptor
                                                                                                                                                                                                                                                                                  Score 69.2; DB 9;
Pred. No. 4.2e-05;
                                    Claim 1; SEQ ID NO 1513; 28pp; English
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98US-0085537P.
98US-0085696P.
98US-0105234P.
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                                                                                                                                                                                                                                                                                                                         Matches 161; Conservative
                                                                                                                                                                                                                                                                                                        Similarity
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15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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                                                                                                                           J, Innis MA, Garcia PD, Sudduth-Klinger J;
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide library used to determine cancerous states of mammalian
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Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
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HYSEQ INC.
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and or avide and or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP, s), and (ii) for differentiation of call or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously, ABQ13410-
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                    Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
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05-SEP-2000;
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ABG54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the
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diagnosis and prognosis, com
from chemically treated DNA.
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                                                                          Score 68.4; DB 6; Length 712;
Pred. No. 4.1e-05;
0; Mismatches 217; Indels
                       Sequence 712 BP; 47 A; 456 C; 181 G; 12 T; 0 U; 16 Other;
                                                                             tch 6.9%; al Similarity 48.6%; 208; Conservative (
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert genomic sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic CD NA that contains the target C is amplified to form a labeled amplicon. The amplicon is hypridised to two classes, each with at least one member, of oligomucleotides and/or peptide-nucleic acid (PNA) oligomers and the amplicon. From the ratio of lasses is determined from the label on the amplicon. From the ratio of lasses is determined from the label on oligomers, the degree of methylation is calculated. The method is used:

(1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastroinestinal and respiratory systems etc. Darticularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation and any or residues to be determined simultaneously. ABD13410-
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05-SEP-2000; 2000DE-01044543.
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                                                                                                                                                                                                                          Query Match 6.9%; Score 68.4; DB 6; Length 712; Best Local Similarity 48.6%; Pred. No. 4.1e-05; Matches 208; Conservative 0; Mismatches 217; Indels
                                                                                                             Sequence 712 BP; 12 A; 181 C; 456 G; 47 T; 0 U; 16 Other;
disclosure of the invention
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Search completed: March 25, 2004, 10:25:05 Job time: 1027.24 secs

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TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 152331
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Sequence 50, 7
Sequence 8, Ap
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/FUTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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Sequence 42, Appl
Sequence 629, App
Sequence 12, Appl
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Sequence 7, Appli
Sequence 842, Ap
Sequence 37, Appl
Sequence 77, Appl
Sequence 77, Appl
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                                                            Sequence 8
Sequence 3
Sequence
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Pred. No. 0.00041;
0; Mismatches 163; Indels 2;
US-08-306-691B-14
US-09-209-668-10
US-09-356-952-8
US-08-406-030A-3
US-09-103-840A-1
US-09-283-471A-7
US-09-283-471A-37
US-09-283-471A-37
US-09-283-471A-37
US-09-281-471A-37
US-09-280-132-77
US-09-990-140-1
US-09-990-140-1
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US-07-745-206A-12
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LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 50.6%;
Matches 169; Conservative (
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GENERAL INFORMATION:
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APPLICANT: Lees, Robert S.
APPLICANTION: PATHEROSCIENS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIENSOIS
FILE REFERRNCE: 10797-004001
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 1997-11-26
PRIOR PILICATION NUMBER: US 60/031,930
PRIOR PILICATION NUMBER: US 60/031,930
PRIOR PILICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1997-11-27
PRIOR PILING DATE: 1997-11-27
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
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                        945 GICCGIGCGCGAGGGCGCCGCGAGCCGICICGG 978
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US-09-91-211-10
Sequence 10, Application US/09791211
; Patent No. 6448080
                                                                                                                                                                             Sequence 48, Application US/09616289 Patent No. 6632923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 52.2
Matches 180; Conservative
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/ LOCATION: (246)...(1895)
US-09-616-289-48
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13404 CCGGGCCCGGCTCCCCCCGGCCCCGCAGCGCGGGCTCCAGCCACTGCCGGCTGGCGGTTGGCG 13463
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APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Wart
TITLE OF INVENTION: ANTISENSE MODULATION OF WEN EXPRESSION
FILE REPERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
LENGTH: 98844
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Patent No. 6197510
GENERAL INFORMATION:
APPLICANT: VINDAGEMOCITHY, Thuralayah
ITILE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER; US/09/165, 264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: 24962
OCHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 64183
OCHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65468
OCHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65468
OCHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65469
OCHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65469
OCHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65470
OCHER INFORMATION: unknown
NAME/KEY: unsure
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LOCATION: 87130
OTHER INFORMATION: unknown
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: 89049
OTHER INFORMATION: U
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OTHER INFORMATION:
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Best Local Simil
Matches 126; C
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US-09-791-211-10
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                                                                                                   880
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEROSIS
FILE REFERENCE: 10797-00407-04
CURRENT PLING DATE: 2000-07-14
FRIOR APPLICATION NUMBER: US 09/517,849
FRIOR APPLICATION NUMBER: US 08/379,608
FRIOR APPLICATION NUMBER: US 60/031,930
FRIOR PLING DATE: 1997-11-27
FRIOR PLING DATE: 1997-11-27
FRIOR PLING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1614
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                                                Length 1614;
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5.7%; Score 56.6; DB 4;
Best Local Similarity 47.5%; Pred. No. 0.00039;
Matches 200; Conservative 0; Mismatches 219;
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US-09-616-289-45
; Sequence 45, Application US/09616289
; Patent No. 6612923
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                                                                                                     FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-13
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Pred. No. 0.00021;
0; Mismatches 164; Indels (
                                                                                                                                                                                                   Length 320;
                                                                                                                                                                                                 Score 57.2; DB 3; Length 3
Pred. No. 0.00015;
0; Mismatches 163; Indels
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Best Local Similarity 48.6%;
Matches 155; Conservative (
                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                      Query Match
Best Local Similarity 48.7%;
Matches 155; Conservative
     SEQ ID NO 13
LENGTH: 320
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A OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-8
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APPLICANT: Leopardi, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
NUMBER OF SEQUENCES: 2
CORRESSONDENCE ADDRESS:
ADDRESSES: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                      APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
FULRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 8
LENGTH: 319
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Patent No. 5876923
GENERAL INFORMATION:
                                                                                                                                                                                                        US-09-165-264-8/c
; Sequence 8, Application US/09165264
; Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 48.6%;
Matches 152; Conservative
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COMPUTER READABLE FORM:
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COUNTRY:
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TGGCTCTCTCGCGCTCTCTCGCTCTCAGGGCCCCCCTCGCTCCCCCGGGCCGCAGTCCGTG 951
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SEQUENCE SU, APPLICATION:
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Anibal A.
TITLE OF INVENTION: NOTEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION: ATHEROSCIEROSIS
TITLE OF INVENTION: ATHEROSCIEROSIS
CURRENT APPLICATION NUMBER: US 09/517, 849
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PELING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 53 606
SROFWARE: FRASESE FOR VAINGOWS Version 4.0
SEQ ID NOS: 53 605
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ORGANISM: Homo sapiens
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US-08-843-659-1
| Sequence 16, Application US/08843659
| Patent No. 618103
| APPLICANT: Leopardi, Roasrio
| APPLICANT: Leopardi, Roasrio
| APPLICANT: Leopardi, Roasrio
| TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
| TITLE OF INVENTION: | INHIBITORS OF APOPTOSIS
| NUMBER OF SUGURNES: 6
| CORRESPONDENCE ADDRESS: | ADDRESSES: | ADDRESSES: | ATREET: PO. Box 4433 |
| CITY: Houston STATE: Texan
                                                                                                                                                                                                                             5.6%; Score 55; DB 3; Length 425 illarity 46.5%; Pred. No. 0.0014; Conservative 0; Mismatches 205; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
FILLING DATE: CONCUR
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NAME: Highlander, Steven L.
REGISTATION NUMBER: 37,642
REPRENCE/DOCKET NUMBER: AKSB:519
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                      ; TYPE: DNA; ORGANISM: HERPES VIRUS, TYPE US-09-259-821A-1
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COUNTRY: United States
ZIP: 77210
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Best Local Similarity
Matches 178; Conserva
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APPLICANT: LEOPARDI, ROSARIO
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
FILE REPRENCE: ARCD:317
CURRENT APPLICATION WIMBER: US/09/259,821A
CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION WIMBER: 08/690,473
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
LENGTH: 4257
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Best Local Similarity 46.5%; Pred. No. 0.0014;
Matches 178; Conservative 0; Mismatches 205; Indels
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTRARE SYSTEM: PC-DOS/MS-DOS

SOFTRARE PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

ATDOMANE: US/08/690,473

FILING DATE: 26-JUL-1996

CLASSIFICATION: 435

ATTOMANY/AGENT INFORMATION:

REGISTRATION NUMBER: 37,642

REPRENCE/DOCKET NUMBER: 37,642

REPRENCE/DOCKET NUMBER: 37,642

REPRENCE/DOCKET NUMBER: 37,642

TELEPHONE: 512/418-3000

TENGTH: 4257 base pairs

TYPE: muclei caid

STRANDEDRESS: single
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US-09-259-821A-1
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4310 CCTGGGCCCCGCGCGCCGCGGGACCCGCGCCTGCCGAGCTCCGCGGCCGCCGCCGCCGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1130 GCGCAAGAGTCCCGGCCCCGGCCCGGCCGGAGGCGCGGCGGCCGCGGACGCCCCCGAAGAC 4071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 GCTGGGTCCGCGGCCGCCCGCCTGCCCGCGCTGCCGCCGGCTCCTGGAGCCAGCGAG 719
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US-09-165-264-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.6%; Score 55; DB 1; Length 12001; Best Local Similarity 46.5%; Pred. No. 0.0021; Matches 178; Conservative 0; Mismatches 205; Indels
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Pred. No. 0.00062;
0; Mismatches 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM; Herpes simplex virus
STRAIN: Herpes Simplex Virus Type 1
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US-09-165-264-11/C
US-09-165-264-11/C
Sequence 11, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
     (215) 568-3100
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Best Local Similarity 48.5%;
Matches 150; Conservative
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                                                                                                                                                                                                                     : 12001 base pairs
nucleic acid
EDNESS: double
                                               TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                     LENGTH:
TYPE: nu
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US-08-458-568A-11/c
is Sequence 11, Application US/08458568A
parence 11, Application US/08458568A
parence 11, Application US/08458568A
parence 11, Applications
represent scheffer, Priscilla A.
APPLICANT: Scheffer, Compositions and Methods for Treatment of Herpesvirus
TITLE OF INVENTION: Infections
T
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                                                                                                                                                                                                                                                                                      Length 4257;
                                                                                                                                                                                                                                                                           Score 55; DB 3; Length 425
Pred. No. 0.0014;
0; Mismatches 205; Indels
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APPLICATION NUMBER: US/08/458,568A
FILING DATE: 02-UNE-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
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NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFCI-0029
TELECOMMUNICATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.5%;
Matches 178; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                          ; TOPOLOGY: linear
US-08-843-659-1
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                          Sequence 7, Application US/08335865J
Patent No. 6107472
GENERAL INFORMATION:
APPLICANT: Stacker, Steven A.; Hovens, Christopher M.,
APPLICANT: Wilks, Andrew F.
TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00210
FILING DATE: 10-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL2358
FILING DATE: 11-May-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII/Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,865J
FILING DATE: 19-January-1995
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REFERENCE/DOCKET NUMBER: LUD-52
TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: single
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COUNTRY: USA
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     US-08-335-865J-7/c
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689 GCTGCCGCCGCCGGGTCCTGGAGCCAGCGAGGGGGGGGGCGGCGCTGCGCTTGCCCGGG
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US-09-165-264-12
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48.7%; Pred. No. 0.00069;
tive 0; Mismatches 156; Indels
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Patent No. 6197510
GRNEAL INFORMATION:
TITLE OF INVENTION: Milti-Loci Genomic Analysis
FILE REFERENCE: 44777
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT APPLICATION NUMBER: US/09/165,264
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
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ORGANISM: Aztificial Seguence
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US-09-165-264-12/c
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LENGTH: 318
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Job time : 200.942 secs

Sequence 10475, A Sequence 10475, A Sequence 113781, Sequence 11845, A Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 1189, Ap Sequence 2910, A Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 2320, Appl Sequence 2320, Appl Sequence 2320, Appl Sequence 5239, Appl Sequence 5239, Appl Sequence 529, Appl Sequence 59, Appl Sequence 6, Appli

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212 creccarrecaarecaececerrrecrrrreaarecarracaecereeececaraarra 271
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8 721 12 US-10-424-599-139811

6 51657 15 US-10-057-475B-10475

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5 14779 12 US-10-148-806-313788

5 14793 14 US-10-148-806-3

6 15 12 US-10-327-472A-1

5 452 14 US-10-327-472A-1

5 452 14 US-10-317-161-1481

5 545 15 US-10-292-98-1189

8 10 12 US-10-424-599-25310

2 3133 15 US-10-424-599-25310

2 3133 15 US-10-017-161-1483

3 133 15 US-10-029-78-1181

1 152331 13 US-10-029-78-1181

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2 561 12 US-10-03-523-48

10 2561 13 US-10-03-523-48

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12 US-10-424-599-54839
9 US-09-954-456-292
9 US-09-954-456-529
9 US-09-880-107-3950
13 US-10-026-188-6
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JOS-09-963-263-6

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JOS-09-963-263-6

JOS-09-963-265-6

JOS-09-963-265-6

JOS-09-963-265-6

JULIE OF INVENTION: PROMOTER SEQUENCES

FILE REPERENCE: 1342-64200

JULIE OF INVENTION: PROMOTER SEQUENCES

FILE REPERENCE: 1342-64200

JULIE OF INVENTION: PROMOTER SEQUENCES

FILE REPERENCE: 1342-64200

JOURRENT FILING DATE: 2001-09-26

PRIOR PILING DATE: 2000-11-09

PRIOR PILING DATE: 2000-11-09

PRIOR PILING DATE: 2000-10-10

PRIOR FILING DATE: 2000-10-10

PRIOR FILING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 24

SOFTHARE: PASELSEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 8

LENGTH: 3289
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2512
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ORGANISM: Homo sapiens
US-09-963-285-8
            RESULT 1
US-09-963-285-8
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Sequence 1, Appli
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 10475, A
Sequence 10475, A
Sequence 1403, Ap
Sequence 1813, Ap
Sequence 1813, Ap
Sequence 1813, Ap
Sequence 1813, Ap
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                                                                                                                                                                           March 25, 2004, 10:03:04; Search time 854.12 Seconds (without alignments) 4297.861 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                     1 ctgccattccaatccagcgc......gagccgtctcggaagcagca 986
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US60_NBW_PUB.seq:*
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-116-265-16
US-10-124-599-61903
US-10-057-475B-10475
US-10-017-484B-10475
US-10-017-161-1403
US-10-022-798-1513
US-10-027-798-1513
US-10-023-393-47
US-10-032-393-47
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US-09-963-285-1
US-09-963-285-5
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1730 AACTITICCCAAICCCTAAAAGGGACTIGGCCTCTTITICIGGCCTCAGGGGGGCAGCCG 1789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1250 CTGCCATTCCAATCCAGCGCGTTTGCTTTTGAATCCATTACACTGGGCCCCCATAATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGCTCCTCGCCCCGATTGGCCCCCGGACTCCTCTCAGCTGCCGGGTGATTGGCTCAAAGT
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100.0%; Score 986; DB 9; Length 6
Best Local Similarity 100.0%; Pred. No. 1.9e-241;
Matches 986; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 2E 0004102-0
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-10-10
PRIOR PILING DATE: 2000-10-10
PRIOR PILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PREUSEQ for Windows Version 4.0
SCOID NO.
                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (2235)...(3737)
US-09-963-285-1
                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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RESULT 2
US-09-963-285-1
Sequence 1, Application US/09963285
Fatent No. US20020090707A1
GENERAL INFORMATION
APPLICANT: Enerbck, Sven
APPLICANT: Rrook, Katarina
APPLICANT: Rondahl, Lena
APPLICANT: Rondahl, Lena
APPLICANT: Rondahl, Lena
TITLE OF INVENTION: PROWOTER SEQUENCES

FILE REFERENCE: 13425-042001

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Db 1970 AGGGGGCCGGCGCTGCGCTTGCCCGGGGCGCCCTCCAGGATGCCGATCCGCCGGTC 2029 Qy 781 cgcTGAAAGGGGGGGCCCTGCTCGGCCCGAAGGACGAAGACGGCACCTCGCCCCGG 840	Db 2030 GGCTGAAAGCGCGCGCGCCCTGCTCGCTCGAGCGACGACGACGCGCGCACGCTCCTCGCCCCGG 2089	Qy 841 AGGCTGCCAGAGACCGGGCCGCCCCTCCCGCTCCCCTCTCCCCTCTGGCTCTCT 900	Db 2090 AdderdechdaAdaAccadaccaccerrecacaccerecereceereceere	901 GGGGTCTCTCGCTCTCAGGGCCCCCTCGCTCCCCGGGCGCGCAGTCCGTGCGCGAGGGC	Db 2150 GGGGCTCTCGCTGCTCAGGGCCCCCCTCGCGCCGGCGGCAGTCGGTGCGCGAGGGC 2209 Qy 961 GCGGGCGAGCGTCTCGGAAGCAGCA 986	Db 2210 GCCGGCGAGCCGTCTCGGAAGCAGCA 2235	RESULT 3	US-09-963-285-5 ; Sequence 5, Application US/09963285 ; Patent No. US20020090707A1	; GENERAL INFORMATION: ; APPLICANT: Enerbok, Sven ; APPLICANT: Enerbok, Sven ; APPLICANT: Enerbok, Sven	; APPLICANT: Rondahl Lena : APPLICANT: Wasserman Work	NVENTION: PR ENCE: 13425- PLICATION NU	; CURRENT FILING DATE: 2001-09-26 ; PRIOR APPLICATION NUMBER: 8D 0004102-0		APPLICATION NUMBER: SE 0003435-5 FILING DATE: 2000-09-26 OF SEQ ID NOS: 24	; SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5 . TEMETH. 6021		; FEATURE: . NAME/KEY: exon ; LOCATIOS. (1649)(438) US-09-963-285-5	29.4%; Score 290; DB	Pred. No. 2.5e 0; Mismatches	Cy 23 TIGCTITIGAALCCATIACACCTGGGCCCCCATAATTAGGAAATCTAATTATCGCTTCA 82	83 TCACTCATTAATAAGAAAAATGTCCCAGGATCATTGCTACTTACAAGGTCTTT	1205 TCATCCATTAATAATAAAAAAAATCTCCAGGCTCTTTCCTACTTACAAGGTCTTG	OY 136 GGGAGGARTITIACTCTATTAATCCATTTTTATATTTCAAATTGAT 187 Db 1265 GGGCAAATCTCTGCCCAACTTCATCAATTCGATGTTATATTTCAAACTAAACTTTT 1324		Qy 188 TITITIAACAGAGAAAGIGGCIATCITITIGITITIGGGGATGIGGGCCCATICACCAA 247	188 TITITIAACAGAGGAAAGIGGCIAICITITIGITITIGGGAIGIGGGCCATTCACCAA	188 TITITIAACAGAGGAAAGIGGCIAICITITIGITITIGGGAIGIGGGCCATICACCAA 1325 TATITICCAAAGGAACAGGGTITITAATITITIGCICIGGACCAGGGGCCATICAAACAA 248 AAIGIGAICATAAAAATITIAAAAAAAACTITICAAGIGA	188 TITITIAACAGAGGAAAGIGGCIAICITITIGITITIGGGAIGGGGCCATICACCAA 1325 TATTICCAAAGGAACAGGTITITAATITITGCTCTGGACACGTGGTCTCGTTAACAA 248 AAIGIGAICATAAAATAAATITITAAAAACTITITAAAAAGITTITCAAGIGA 1385 AAIGIGAICATAAAATAAAATITITATAAAGITGTAAACGIGA

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0
               Length 805;
                                                                                       Indels
       Score 74.2; DB 12;
Pred. No. 1.4e-08;
0; Mismatches 195;
   7.5%;
       Query Match
Best Local Similarity 49.0
Matches 187; Conservative
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalid David K
APPLICANT: Kovalid David K
APPLICANT: Avalid David K
APPLICANT: Avalid David K
APPLICANT: Avalid William
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                   921 GCCCCCCTCCCCCCCCCGCGCGCAGTCCGTGCGCGAGGGCGCCGCGGGAGCCGTCTCGGAA
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82.7%; Pred. No. 2.1e-09;
ive 13; Mismatches 0; Indels
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OTHER INFORMATION: unsure at all n locations
FEATURE:
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Sequence 16, Application US/10116265
Publication No. US20030077612A1
GENERAL INFORMATION:
APPLICANT: Ekblom, Jonas
TITLE OF INVENTION: NEW METHOD
FILE REPRENCE: 13425-105001
CURRENT APPLICATION NUMBER: US/10/116,265
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 60/281,384
PRIOR FILING DATE: 2001-04-05
FRIOR APPLICATION NUMBER: 60/281,384
FRIOR APPLICATION NUMBER: 60/281,384
FRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FRSEED for Windows Version 4.0
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52; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Glycine max
                                                                                                                                                                                                                          GCAGC 985
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NAME/KEY: unsure
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LENGTH: 805
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LENGIH: 75
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Best Local S
Matches 62
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17943 CGGGGGCCCCCCCGGCCCGGCCCGGCCCGCGNGCCGGCCCCGCCCCGCCCGCCCGGC
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         PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR PILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOPTHARE: PastSEQ for Windows Version 3.0
ENGTH: 51657
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 51657;
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APPLICANT: SURVA, MAKIKO
APPLICANT: AKIYAMA, YUTKA
APPLICANT: AKIYAMA, YUTKA
APPLICANT: AKIYAMA, YUTKA
APPLICANT: AKIYAMA, YUTKA
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
FILOR PELLING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PARCENTIN VET: 2.1
LENGTH: 1117
TYPE: DNA
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48.9%; Pred. No. 2.2e-07;
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                                                                                                                                                                                                                                                                                                                  | PEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(51657)
| OTHER INFORMATION: n = g, a, c or
| US-10-154-884B-10475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 48.9
Matches 197; Conservative
                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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US-10-017-161-1403/c
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Algate, Paul A.

Algate, Paul A.

APPLICANT: Retter, Marc M.

APPLICANT: Corisa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy,

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy,

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy,

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy,

TITLE OF INVENTION: Composition and Methods for the Detection, Diagnosis and Therapy,

TITLE OF INVENTION: Composition and Methods for the Detection, Diagnosis and Therapy,

TITLE OF INVENTION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR PLICATION NUMBER: US 60/200,303

PRIOR PLICATION NUMBER: US 60/200,303

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR PLING DATE: 2000-04-27

PRIOR PLING DATE: 2000-04-28

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                                                                                                                                                                                                                                                                          Length 51657;
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                                                                                                                                                                                                                                                                     Score 73.6; DB 15; Length
Pred. No. 2.2e-07;
0; Mismatches 203; Indels
NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10475
LENGTH: 51657
                                                                                                                                                        NAME/KEY: misc_feature

LOCATION: (1)...(51657)

COTHER INFORMATION: n = g, a, c or

US-10-057-475B-10475
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                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.9
Matches 197; Conservative
                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                       FEATURE
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FEATURE:
NAME/KEY: modified base
NAME/KEY: modified base
OTHER INFORMATION: a, t, c, g, unknown or other
FRATURE:
NAME/KEY: modified base
NOAMION: (356). (361)
OTHER INFORMATION: a, t, c, g, unknown or other
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COCATION: (173)

THER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
NAME/KEY: modified base
OTHER INFORMATION: a, t, c, g, unknown or other
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OCATION: (343) . (344)
DIHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (431)...(432)
OTHER INFORMATION: a, t, c, g, unknown or other
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OCATION: (437)...(438)
THER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (440)...(444)
CTHER INFORMATION: a, t, c, g, unknown or other
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OCATION: (378)
OTHER INFORMATION: a, t, c, g, unknown or other
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THER INFORMATION: a, t, c, g, unknown or other
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THER INFORMATION: a, t, c, g, unknown or other
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OCATION: (401)...(402)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (434)
OTHER_INFORMATION: a, t, c, g, unknown or other
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THER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (405)
77HER INFORMATION: a, t, c, g, unknown or other
                                                                                                       NAME/KEY: CDS
LOCATION: (201)..(917)
PATURE:
NAME/KEY: modified_base
LOCATION: (170)
                                                                                                                                                                                         LOCATION: (170)
STHER INFORMATION: a, t,
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NAME/KEY: modified_base
ORGANISM: Homo sapiens
                                           source
(1)..(1117)
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PLOCATION: (468)

WHERE THE PROMATION: a, t, c, g, unknown or other PRATURE: modified base

OUTHER INFORMATION: a, t, c, g, unknown or other representations and to the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the properties of the proper
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RESULT 10
US-10-292-798-1141/c
IS Sequence 1141, Application US/10292798
| Sequence 1141, Application US/10292798
| Publication No. US20030235833A1
| GENERAL INFORMATION:
| APPLICANT: SURA, MAKINO
| APPLICANT: ARIYAWA, YUTAKA
| APPLICANT: ARIYAWA, YUTAKA
| APPLICANT: ALWAFMAIN, HIROYUKI
| TITLE OF INVENTIONS: GLANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
| FILE REFERENCE: 084335/166
| CURRENT FILING DATE: 2002-11-13
| PRIOR APPLICATION NUMBER: US/10/292,798
| CURRENT FILING DATE: 2001-12-18
| PRIOR FILING DATE: 2001-12-18
| PRIOR FILING DATE: 2001-06-18
| NUMBER OF SEQ ID NOS: 2070
| SOFTWARE: PatentIn Ver. 2.1
| LEAST OF THE COUPLED RECEPTORS SEQ ID NO 1141
| LEAST OF THE COUPLED RECEPTORS NUMBER: PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATENT PATE
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LOCATION: (173)..(173)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (351)...(356)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (401)..(402)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (360)..(361)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (398)..(399)
OTHER INFORMATION: a, t, c,
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NAME/KEY: modified_base
COCATION: (170)..(170)
OTHER INFORMATION: a, t, c
FEATURE:
NAME/KEY: modified_base
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NAME/KEY: modified base
LOCATION: (207)..(306)
OTHER INFORMATION: a, t,
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LOCATION: (343)..(344)
OTHER INFORMATION: a, t,
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NAME/KEY: modified base
LOCATION: (378)..(378)
OTHER INFORMATION: a, t,
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LOCATION: (380)..(383)
OTHER INFORMATION: a, t,
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ORGANISM: Homo sapiens
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FEATURE:
LOCATION: (1)..(1117)
FEATURE:
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(201)..(917)
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7.4%; Score 73; DB 14; Length 1117;
Best Local Similarity 36.0%; Pred. No. 3.3e-08;
Matches 157; Conservative 0; Mismatches 279; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: modified base
LOCATION: (673)..(675)
OTHER INFORMATION: a, t, c, g, unknown or other
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (650)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (694)..(696)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (652)..(653)
OTHER INFORMATION: a, t, c,
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NAME/KEY: modified_base
LOCATION: (688)..(689)
OTHER INFORMATION: a, t, c,
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                                                                                      NAME/KEY: modified_base
LOCATION: (646)
OTHER INFORMATION: a, t,
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THER INFORMATION: a, t,
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LOCATION: (648)
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LOCATION: (698)
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NAME/KEY: modified base

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LOCATION: (405)(405) OTHER INFORMATION: a, t, c,	FALUE: NAME/KEY: modified base LOCATION: (431)(432) OTHER INFORMATION: a, t, C,	FEALONE: NAME/KEY: modified base LOCATION: (434)(434) OTHER INFORMATION: a, t, c,	FEATURE: NAME/KES: LOCATION: (437)(438) OTHER INFORMATION: a, t, c,	FEATURE: NAME/KEY: modified base LOCATION: (440)(444) OTHER INFORMATION: a, t, c,	FEATURE: NAME/KEY: modified_base LOCATION: (464)(465) OTHER INFORMATION: a, t, c,	FEATURE: DAME/KEY: LOCATION: (468)(468) OTHER INFORMATION: a, t, c,	FEATURE: NAME/KEY: modified base LOCATION: (484)(484) OTHER INFORMATION: a, t, c,	FALLOWS: NAME/KEY: modified base LOCATION: (487)(497) OTHER INFORMATION: a, t, c,	FAILORE: FAMILY KEY: modified base LOCATION: (509)(510) OTHER INFORMATION: a, t, c,	FEATURE: NAME/KEY: NAME/KEY: COCATION: (525)(527) OTHER INFORMATION: a, t, c,	FEATURE: NAME/KE: LOCATION: (532)(533) OTHER INFORMATION: a, t, c,	FEATURE: NAME/KEY: LOCATION: (539)(542) OTHER INFORMATION: a, t, c,	FEATURE: NAME/KEY: modified base LOCATION: (548)(548) OTHER INFORMATION: a, t, c,	FEALURE: DAMB/KEY: modified base LOCATION: (552)(552) OTHER INFORMATION: a, t, c,	FALUNE: NAME/KEY: modified base LOCATION: (557)(561) OTHER INFORMATION: a, t, C,	FALLORE: NAME/KEY: MANE/KEY: MANE/KE	FEATURE: LOCATION: (573). (573) OTHER INFORMATION: a, t, c,	FEATURE: NAME/KEY: modified base LOCATION: (577)(577)

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541 CTCGGACCCCGGCGCGCTGACCCTCGGGGCTGCCGATTCGCTGGGGGCTTGGAGAGCCTC 600
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                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: modified base
LOCATION: (617)...(617)
OTHER INFORMATION: a, t, c, g, unknown or other
PEATURE:
NAME/KEY: modified base
LOCATION: (619)...(622)
OTHER INFORMATION: a, t, c, g, unknown or other
NAME/KEY: modified base
LOCATION: (629)...(629)
OTHER INFORMATION: a, t, c, g, unknown or other
NAME/KEY: modified base
LOCATION: (629)...(629)
OTHER INFORMATION: a, t, c, g, unknown or other
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (688)...(688)...
OTHER INFORMATION: a, t, c, g, unknown or other
FRATURE:
NAME/KEY: modified base
LOCATION: (694)...(696)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                      FEATURE:
NAME/KEY: modified base
LOCATION: (605). (610)
OTHER INFORMATION: a, t, c, g, unknown or other
PEATURE:
NAME/KEY: modified base
LOCATION: (615). (615)
OTHER INFORWATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (648)...(648).
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (650)...(650)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
NAME/KEY: modified base
OCATION: (646). (646)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (652)..(653)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (673)..(675)
OTHER INFORMATION: a, t, c, g, unknown or other
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (669)..(669)
FEATURE INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (588)..(589)
OTHER INFORMATION: a, t,
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LOCATION: (1130)
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NAME/KEY: modified base
LOCATION: (1105)..(1107)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (1066)...(1067)
OTHER INFORMATION: a, t, c,
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NAME/KEY: modified base
LOCATION: (1082)...(1084)
OTHER INFORMATION: a, t, c,
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LOCATION: (920)
OTHER INFORMATION: a, t, c,
FEATURE:
NAME/KEY: modified_base
LOCATION: (941)
OTHER INFORMATION: a, t, c
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THER INFORMATION: a, t,
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LOCATION: (754)..(756)
OTHER INFORMATION: a, t,
FEATURE:
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NAME/KEY: modified base
LOCATION: (750)
OTHER INFORMATION: a, t,
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LOCATION: (761)
OTHER INFORMATION: a, t,
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LOCATION: (763)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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LOCATION: (843)
OTHER INFORMATION: a, t,
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LOCATION: (897)
OTHER INFORMATION: a, t,
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LOCATION: (752)
OTHER INFORMATION: a, t,
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LOCATION: (995)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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                                                                                       Sequence 1857, Application US/10017161
Fublication No. US20030143668A1
Fublication No. US20030143668A1
FUBLICANT: WURA, MAKKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
FRIOR APPLICATION NUMBER: US/2001/246789
FRIOR APPLICATION NUMBER: US 2001/246789
FRIOR FILING DATE: 2010-06-18
FRIOR APPLICATION NUMBER: US 2010/246789
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NAME/KEY: Source
LOCATION: (1)..(3163)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2963)
FEATURE:
NAME/KEY: modified base
LOCATION: (556)..(655)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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NAME/KEY: modified base
LOCATION: (709)..(736)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (739)..(743)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (671)...697)
OTHER INFORMATION: a, t, c, g, unknown
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NAME/KEY: modified base
LOCATION: (704)..(707)
OTHER INFORMATION: a, t,
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ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: modified base
LOCATION: (1247)..(1248)
OTHER:INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c,
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NAME/KEY: modified base
LOCATION: (1866)..(1965)
OTHER INFORMATION: a, t, c,
NAME/KEY: modified_base
LOCATION: (1147)
OTHER INFORMATION: a, t, C,
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LOCATION: (1852)
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NAME/KEY: modified_base
LOCATION: (1162)
OTHER INFORMATION: a, t,
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OCATION: (1635)
THER INFORMATION: a, t,
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LOCATION: (1500)
THER INFORMATION: a, t,
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APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIVOSHI
APPLICANT: ASAI, KIVOSHI
APPLICANT: ASAI, KIVOSHI
APPLICANT: ASIYAMA, YUTAKA
APPLICANT: ASURATANI, HIROYUKI
ITLE OF INVENITON: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REPERBNCE: 084335/166
CURRENT FILING DATE: 2002-11-13
FRIOR PELICATION NUMBER: 10/017,161
PRIOR PLILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
SOFTWARER OF SEQ ID NOS: 2070
SOFTWARER PAGENTIN Ver. 2.1
SEQ ID NO 1513
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LOCATION: (1968)..(1980)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATUME.
FEATUME.KEY: modified base
LOCATION: (1982)..(2009)
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NAME/KEY: modified_base
NAME/KEY: (658).(669)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (556)..(655)
OTHER INFORMATION: a, t, c,
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LOCATION: (201)..(2963)
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ORGANISM: Homo sapiens
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LOCATION: source
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LOCATION: (1)..(3163)
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llarity 48.4%; Pred. No. 4.2e-06;
Conservative 0; Mismatches 198;
                                                                                                                                                             6.8%; Score 67.4; DB 12; 47.1%; Pred. No. 7.3e-07;
                                                                                                                                                                                                                                                                                                                           0; Mismatches 184;
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Publication No. US20030027286A1
GENERAL INFORMATION:
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US-10-032-393-47
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                                                                                                                                                             Query Match 6.8
Best Local Similarity 47.1
Matches 164; Conservative
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US-10-032-393-47/c
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Best Local S
Matches 186
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US-10-424-599-107958/C
Sequence 107958, Application US/10424599
Sequence 107958, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Acvalic David K
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
SEQ ID NO 107958
LENGTH: 771
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LOCATION: (1)..(771)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_68501C.1
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NAME/KEY: modified base
LOCATION: (1968)...[1980)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (1695)..(1695)
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LOCATION: (1866)..(1965)
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Best Local Similarity 45.7%;
Matches 161; Conservative
LOCATION: (1674)...(1674)
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APPLICANT: Gross, Molly
FILLE OF INVANION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA, 010A
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2000-12-7
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR APPLICATION NUMBER: 09/048,993
PRIOR APPLICATION NUMBER: 09/048,993
PRIOR PLING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 12739
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Publication No. US2030027286A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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ORGANISM: Artificial Sequence
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Drosophila melanogaster genome survey sequence T7 end of BAC # BACK14809 of RPCT-98 library from Drosophila melanogaster (fruit AL066742 AL066742 Giry 1995265
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Submitted (12-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr.)
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfiy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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(bases 1 to 1201)

Li, W.B., Gruber; C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                         /organism="Pristionchus pacificus"
/mol type="genomic DNA"
/strain="california"
/db xref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector."
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 0447071601371
Eax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
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larity 55.3%; Pred. No. 6.5e-07;
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BRT14B09"
/clone_lib="RRCI-98"
/note="end : T7"
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                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCC/Dcrp/Drp
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM12332 row; 1 column: 22
High quality sequence stop: 294.
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                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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52.0%; Pred. No. 1.9e-06;
tive 0; Mismatches 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cSoD1080vp07"
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/clone_Tib="PLACRYTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tist strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                           Enail: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4309.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CSODIO80CCG4NPI&cluster=4309.f. Contact :
Feng Liang Email : fliang@lifetech.com UNL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO80CCG4NPI.
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44.0%; Pred. No. 1.2e-06;
tive 57; Mismatches 202; Indels 2;
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191 91006 EVRY cedex - France
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GI:30529403
                         Gallus gallus (chicken)
Gallus gallus
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CCH261-185P7 Sp6.2 CH261 Gallus gallus genomic clone CH261-185P7,
genomic survey sequence.
CC210735
                            1 (bases 1 to 1406)
Stintyasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.
An inteagrated physical and genetic map of the nematode Pristionchus
pacificus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
vector."
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  Chromadorea; Diplogasterida;
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Pred. No. 2.7e-06;
0; Mismatches 231; Indels
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Max-Planck-Institute for Developmental Biology
Spemannstr. 3-39, Tuebingen D-72076, Germany
Tal: 00497071601371
Fax: 00497071601498
                                                                                      Mol. Genet. Genomics 269 (5), 715-722 (2003)
22835951
                                                                                                                                                                                                                                                    1. .1406
Corganism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                               Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
 Eukaryota, Metazoa, Nematoda, Chi
Neodiplogasteridae, Pristionchus
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/clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_l: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - For library and clone
ordering information: http://www.chori.org/bacpac"
CAGGATGCCGATCCGCCCGGTCCGCTGAAAGCGCGCCCCCTGCTCGGCCCCGAGCGACGA
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 71
High quality sequence stop: 159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.5%; Score 93.2; DB 28;
Best Local Similarity 51.3%; Pred. No. 4.6e-06;
Matches 235; Conservative 0; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/strain="Red_Jungle_Fowl"
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/clone="CH261-185P7"
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/organism="Gallus gallus"
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/ Use in the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the interior of the i
                                                                                                                                                                                                                  1046 bp mRNA linear EST 21-AUG-2002 5', mRNA sequence.
BQ552554.1 G1:22368032 EST.
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I (bases I to 1046)

NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can letus://image.llnl.gov
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764 SSCCSGGCGCCEXTGCGCKCCKCGMAAAAMCCCCCCCCCCCCCCCMMMMMMC 714
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Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9016.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq-CSSCAP008CD01QP1&cluster=9016.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://tullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP008CD01QP1.
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Best Local Similarity 39.4%; Pred. No. 5e-06;
Matches 162; Conservative 76; Mismatches 172; Indels
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
/clone="CSOCAP008YH01"
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Mammalia; Eutheria; Primates;
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Lotoki, Y., Hattozi, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Matanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEM), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:chimpbesgagc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Was generated during the R&D process and may have higher chance of
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Pan troglodytes (chimpanzee)
Buhar troglodytes
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                           948
                                                                     771 CCGCCCGGTCCGCTGAAAGCGCGCCCCTGCTCGGCCCGAGCGACGACGACGCGCACC
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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48.1%; Pred. No. 8.1e-06;
tive 0; Mismatches 240;
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/mol type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-139G20.R"
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Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

El (bases 1 to 1016)

National Institutes of Health, Mammalian Gene Collection (MGC)

Mutional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

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Contact: Robert Strausberg, Ph.D.

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Contact: Preparation: Life Technologies, Inc.

Contact Preparation: Life Technologies, Inc.

Contact Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be thus: //image.lln.gov

Plate: LLAM13895 row: 1 column: 11

High quality sequence stop: 407.

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//organism="mmsmm:"
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IMAGE:6397594 5', mRNA sequence.
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/db.maref=rexon:10090"
/clone="INAGE:6397594"
/lab_host="DH10B (T1 phage-resistant)"
/clone=lib="NCI CGAP Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidix ecitonally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/strain="FVB/N"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2004 row: b column: 13
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High quality sequence stop: 206.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5480748"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lat strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.ons.fr, www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7092.r For
more information about this cluster, see
http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CSOBAH015ZB03NP1&cluster=7092.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://tullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAH015ZB03NP1.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Frull-length cDNA libraries and normalization
Unpublished (2001)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1063YK05"
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Incre="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E (Dases I to 716)

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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone="BACR14B09"
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/_clone_lib="Homo saplens PLACENTA"
/_clone_lib="Homo saplens PLACENTA"
/_note="Wector: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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BX464554 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE007YB11
3-PRIME, mRNA sequence.
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279 GTCGGCTGAACCCGAGCGCCGGCGTCTTCCGCG-----CGTGGACCGCGAGGCTGCCCCG 3333
                                                                                                                                                                             Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BEmail: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3370.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSIDE002ZF03NP1&cluster=3370.r. Contact :
Frog Library Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSIDE002ZF03NP1.
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Catarrhini; Hominidae; Homo.
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larity 38.8%; Pred. No. 1.5e-05;
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1 (bases 1 to 807)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE007YB11"
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		Description	Abi69613 Oligonucl	Aat74184 Salmonell	Ack23905 Human mic	_	Aav26158 FIV gag-p	н	2 Felin	80	ო	Aac98261 Human col	e Mouse	3 Human	Abs49281 Human liv	œ	Abx60874 Arabidops		m	Abz71640 Breast sp	4	8 Human	Aas34006 Human cDN	'n	Abv34717 Human pro
SUMMARIES		ID	ABI69613	AAT74184	ACK23905	AAV26241	AAV26158	AAZ34901	AAL46912	AAL30218	AAF77183	AAC98261	AB199496	ABA75013	ABS49281	ABV07368	ABX60874	ABV18575	AAC21173	ABZ71640	AAL25924	ABA13678	AAS34006	AAC35275	ABV34717
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	ж (Vuery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastroinrestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC99989, ABF0010-ABF99899 ABR0010-ABF99899 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but

Claim 1; SEQ ID NO 369586; 29pp + Sequence Listing; German.

Abv43572 Human pro	Abq57116 Human col	Acf69945 Photorhab	Acf68904 Photorhab		Aca00439 C. glutam		Abt10067 Human bre	Aac22582 Human sec	Aaz42754 Human 5'	Aag60407 Human bra	Aball183 Human ner		Abn20059 Human ORF	Aai88509 Human pol	Abl63559 Breast ca	Abl63976 Breast ca	Aaa16021 Human col	4	Aai84963 Human pol	Aaa30901 Breast ca	Ade61417 Rat gene
ABV43572	ABO57116	ACF69945	ACF68904	AAV86663	ACA00439	ABV48358	ABT10067	AAC22582	AAZ42754	AA060407	ABA11183	AA182851	ABN20059	AA188509	ABL63559	ABL63976	AAA16021	AAI93544	AAI84963	AAA30901	ADE61417
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273	273	273	273	282	291	301	310	321	324	338	348	351	354	355	355	355	361	364	374	376	378
100.0	100.0	100.0	100	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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24	2,5	36	2,0	, c	0 0) C		22	i m	, t	, 	3 9	7 0	n c o	ָ ס ה ר) C	c 41	42	4	. 4.	45

ALIGNMENTS

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 369586 for detecting SNP TSC0057728. Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. Berlin K; ABI69613 standard; DNA; 12 BP 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. (first entry) Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2001-657177/75. WO200177384-A2. sapiens, 18-OCT-2001. 22-FEB-2002 AB169613; Homo RESULT 1 ABI69613/ pressed sequence tag; microarray; gene expression; biallelic marker; polymorphism; human;

expressed

ВР.

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New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                 Human microarray DNA oligonucleotide SEQ ID NO 123886
                                                                                                                                                                                                                                                                                                                                                                                  claim 1; SEQ ID NO 123886; 9pp; English
                                                                                                                                                                                                                                     16-MAR-2001; 2001US-0276759P
                                                                                                                                                                                                               15-MAR-2002; 2002US-00098263
ACK23905 standard; DNA; 25
                                                                                                                   cross-species comparison.
                                                                                                                                                                                                                                                             (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                            WPI; 2003-567953/53
                                                                                                         genetic variation;
                                                                                             EST; ss; probe;
                                                                                                                                                                 JS2003104410-A1
                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                       dittmann MP;
                                               14-OCT-2003
                                                                                                                                                                                          05-JUN-2003
                        ACK23905;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a PCR primer for the amplification of sefB from Salmonella enteritidis. The nucleic acid produced can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody; polymerase chain reaction; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 12; DB 2; Length 19; 100.0%; Pred. No. 8.7e+03; ive 0; Mismatches 0; Indels
                                                             Length 12;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 4 A; 3 C; 2 G; 10 T; 0 U; 0 Other;
                                   Sequence 12 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 0 Other;
                                                          100.0%; Score 12; DB 5; I
100.0%; Pred. No. 8.7e+03;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                            Salmonella enteritidis sefB PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Col 51; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Doran JL
                                                                                                                                                                                             AAT74184 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                             94US-00233788
                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-00054452
                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                        Local Similarity 100, ses 12; Conservative
                                                                                                           1 GGAAAGTAAAAA 12
                                                                                                                                   12 GGAAAGTAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collinson SK, Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-309886/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1993;
                                                                                                                                                                                                                                           25-MAR-2003
29-SEP-1997
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Matches
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its component match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in maniyais of genetic variation or in hybridisation of anylabrary, or nanalysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring can expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes in situ hybridisation, in Southern, Northern or dotonoles is useful in in situ hybridisation, in Southern, Northern or dotonole and any gene, in mapping the 5' termin of many members of any gene, in mapping the 5' termin of many many of the conditional subclones containing segments of DNA that have been contained and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequence. html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 12; DB 8; 100.0%; Pred. No. 8.7e+03; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV26241 standard; DNA; 28 BP.
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Best Local Similarity
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AAV26241/c
ID AAV26
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Gaps

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12; Conservative 1 GGAAAGTAAAA 12

Matches

14 GGAAAGTAAAAA

RESULT 3 ACK23905/c

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25-JUL-1996;
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                                                                   409804684-A1
                                                                                                                25-JUL-1997;
                                                                                                                                                                                      Cochran MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2000
                                                                                          05-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ34901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a PCR primer from the present invention.

The present invention specifically describes recombinant swinepox virus (SPV) comprising a foreign DNA (I) inserted into a SPV genome which is capable of being expressed in a host cell into which the virus is capable to a 1.2 kb subfragment of the Hindlil K fragment which corresponding to a 1.2 kb subfragment of the Hindlil K fragment which contains both a Hindlil and an BCORI site, of the SPV genome, and contains both a Hindlil and an BCORI site, of the SPV genome, and thindlil to BglII subfragment of the Hindlil M fragment. The recombinant CSPV can be used in a vaccine for immunising an animal against SPV. The invention also provides a method for testing a swine to determine whether convention also provides a method for testing a swine to determine whether convention as the hindlil M recombinate SPV. The seudorables virus. Also (I) inserted into recombinant SPV can be used in a diagnostic assay, e.g. Feline immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis p39 and 22kd are useful to detect feline immunodeficiency caused by FIV and to detect heartworm caused by D. immitis respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                 Recombinant swine pox virus - useful in vaccine for immunising animal against swine pox virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;
                                                                   Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis; pseudorabies virus; feline immunodeficiency virus; FIV; heartworm; Dirofilaria immitis; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIV gag-protease gene PCR primer from WO9804684 Example 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 12; DB 2; Length 28; 100.0%; Pred. No. 8.7e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28 BP; 4 A; 9 C; 4 G; 11 T; 0 U; 0 Other;
                                               FIV gag gene PCR primer from WO9804684,
                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 76; 473pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV26158 standard; DNA; 28 BP
                                                                                                                              Feline immunodeficiency virus
                                                                                                                                                                                                    97WO-US012212.
                                                                                                                                                                                                                          96US-00686968
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Best Local Similarity lov.v.
Best Local 2; Conservative
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                         24-JUL-1998 (first entry)
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                                                                                                                                                                                                                                                                         Cochran MD, Junker DE;
                                                                                                                                                                                                                                                 (SYTR ) SYNTRO CORP.
                                                                                                                                                                                                                                                                                              WPI; 1998-130677/12.
                                                                                                                                                                                                    25-JUL-1997;
                                                                                                                                                                                                                         25-JUL-1996;
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                                                                                                                                                                             05-FEB-1998
                                                                                                                     Synthetic
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   AAV26241;
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The present sequence represents a PCR primer used in an example from the present invention. The present invention specifically describes crecombinant swinnepox virus (SFV) comprising a foreign DNA (I) inserted into a SPV genome which is capable of being expressed in a host cell into which the virus is introduced, where (I) is inserted into: (a) an EcoRI site within a region corresponding to a 3.2 kb subfragment of the HindIII of the HindIII of site within a region corresponding to a 3.6 kb HindIII to BglII subfragment of the HindIII in fragment. The recombinant SPV can be used in a vaccine for immunising an animal against SPV. The invention also provides a method for testing a swine to determine whether the swine has been vaccineted with the vaccine, particularly containing S-SPV-008, or is infected with a naturally containing S-SPV-008, or is infected with a naturally containing S-SPV-008, or is infected with a naturally recombinant SPV can be used in a diagnostic assay, e.g. Peline immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis Immunis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant swine pox virus - useful in vaccine for immunising animal against swine pox virus.
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pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;
Dirofilaria immitis; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 12, DB 2, Length 28; 100.0%; Pred. No. 8.7e+03; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28 BP; 4 A; 9 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIV gag/protase gene PCR primer 11/94.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 44; Page 214; 473pp; English.
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AAZ34901/c
ID AAZ34901 standard; DNA; 28 BP.
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                                                                                                                                                                                                                                        Feline immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-00686968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US012212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGAAAGTAAAAA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Junker DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-130677/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYTR ) SYNTRO CORP.
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The present invention relates to a recombinant virus comprising at least one foreign nucleic acid encoding a protein selected from feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or CTLA-4, which is capable of expression when the virus is introduced into an appropriate host. The virus can be administered to the feline in order to allicit or enhance an immune response to prevent or treat feline in order to immunodeficiency disease, feline leukemia, feline infectious peritonitis, cancers, degenerative and autoimmune diseases and immunodeficiency. The present sequence is a PCR primer described in the exemplification of the invention. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to steaddardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunosuppressive, immunostimulatory, antiinflammatory, cytostatic, neuroprofective, antimirorobial, gene therapy, vaccine, amylase, cancer, amyloid protein; adjopoietin, apoptosis related protein, cadherin, cyclin, polymerase, oncogene, histone, kinase, colony stimulating factor, complement related protein, cytochrome, kinesin; cytokine, interferon, interleukin, G-protein coupled receptor, thiossterase, inflammation, multifactorial disease, autoimmune disease, infection;
                                                        New recombinant virus, useful for immunizing felines to prevent or treat feline immunodeficiency virus, comprises foreign nucleic acid encoding feline cytotoxic T lymphocyte accessory molecules CD28, CD80, CD86 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 12; DB 6; Length 28; 100.0%; Pred. No. 8.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28 BP; 4 A; 9 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                            Disclosure; Page 61; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human SNP oligonucleotide #3426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAL30218 standard; DNA; 48 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000; 2000WO-US035498.
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27-DEC-2000; 2000US-00173419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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12; Conservative
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                     WPI; 2002-415200/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200147944-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL30218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                      CTLA-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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ID AAL3
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                                                                                                                                                                                                                                                                                                                                                                                                     This oligonuclectide represents downstream primer 11/94.10 that was used in the PCR amplification of the FIV gag/protease gene. The primer throthdees a 3' BglIs site into the gene. The amplified gene was used in the construction of homology vector 904-65.B7, which was used to insert fereign DNA into swinepox virus (SPV). The invention relates to a recombinant virus, e.g. SPV, that contains at least one foreign nucleic acid, inserted into a nonessential genomic region, that encodes feline CD28, CD80, CD86 or CTLA-4 protein, or their immunogenic fragments, and is expressed when the recombinant virus is introduced into a suitable host. The recombinant virus may further comprise a foreign nucleic acid encoding an immunogen derived from a feline pathogen such as FIV. It is used to enhance an immune response in a feline, particularly as a vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cat, CD28, CD80, CTLA-4, CD86; immunogen; vaccine; viral infection; feline immunodeficiency disease; feline infections peritonitis; feline leukaemia virus; cancer; degenerative disease; autoimmune disease; virucide; immunomodulator; cytostatic; immunodeficiency; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                 Novel recombinant virus useful as immunomodulators, particularly in
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 12; DB 3; Length 28; 100.0%; Pred. No. 8.7e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 28 BP; 4 A; 9 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                                      (SCHE ) SCHERING-PLOUGH LTD.
(SCHE ) SCHERING-PLOUGH VETERINARY CORP.
                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 60; 230pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL46912 standard; DNA; 28 BP.
                                              99WO-US009504
                                                                                            98US-00071711
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(revised)
(first entry)
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAAGTAAAA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 GGAAAGTAAAA 16
                                                                                                                                                                                                          Winslow BJ, Cochran MD;
                                                                                                                                                                                                                                                      WPI; 2000-062155/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002051792-A1.
                                                30-APR-1999;
                                                                                            01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-2002.
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07-AUG-2003
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                                                                                                                                                                                                                                                                                                                               vaccines
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ઠે d Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.

Leach M;

Shimkets RA,

99US-00303040.

30-APR-1999; 01-MAY-1998;

98US-0083870P

Winslow BJ, Cochran MD;

WINSLOW B J. COCHRAN M D.

(WINS/)

WPI; 2001-465210/50.

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Gaps

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0; Indels

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Gaps

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0; Indels Length

Mismatches

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Conservative

100.0%; Score 12; DB 4; I 100.0%; Pred. No. 8.6e+03;

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was used to determine precisely where on the VRE IRF-7 acts
                           Sequence 58 BP; 31 A; 6 C; 14 G; 7 T; 0 U; 0 Other;
                                                                                                                1 GGAAAGTAAAAA 12
                                                                                                                                            12 GGAAAGTAAAA 23
                                                        Query Match
Best Local Similarity
                                                                                    12;
                                                                                                                                                                                                                                                 AAC98261;
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                                                                                                                                                                                     RESULT 10
AAC98261
                                                                                    Matches
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                                                                                                                                            셤
                        The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apolymorses, oncogenes, histories, kinases, colony stimulating factors, complement related proteins, cadherin, polymerses, oncogenes, histories, kinases, colony stimulating factors, complement related proteins cytochromes, kinesins, cytokines, interferons, interleukins, Grand protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidhey, leukaemia), diseases of the nervous system and an infection of pathogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to controlling the level of Type 1 interferon expression by modulating the level of interferon regulatory factor (IRP)-7 or its functional analogue. This is useful for manufacturing a medicament for treating a condition in which an increase in interferon-alpha is beneficial, such as human viral infections or cancer. The method may also be used in the preparation of DNA vaccines for treating viral, bacterial and parasitic infections. The present sequence is the interferon alpha Al promoter VRE mutant 4PM. This mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Controlling Type I interferon expression level involves modulating level of interferon regulatory factor 7 or its functional analogue which is useful for treating human viral infections or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interferon alpha; IFN; Al promoter; virus responsive element; VRE; interferon regulatory factor; IRF-7; infection; cancer; DNA vaccine; ds.
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                     100.0%; Score 12; DB 4; Length 48; 100.0%; Pred. No. 8.6e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              Sequence 48 BP; 7 A; 9 C; 1 G; 31 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interferon alpha Al promoter VRE mutant 4PM.
   Claim 1; Page 2369; 4143pp; English.
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   1 GGAAAGTAAAA 12
                                                                                                                                                                                                                                                                                                                                                                                             GGAAAGTAAAAA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1999;
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                                                                                                                                                                                                                                                    organisms
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called human colon cancer antigens, given in AAB51234 to AAB54006. The human colon cancer antigens can have cytostatic, cardiacative, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, valnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polymucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such, as colon cancer. The polymucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent disorders such as neural disorders, immune system disorders, wounds, renal disorders, reproductive disorders, immune system cardiovascular disorders, reproductive disorders, immune system cardiovascular disorders, AAC99744 to AAC99772 and AAB54007 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
                                                                                                                                                                                                                                                                                                                                             Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic, antimifective; antibacterial; gene therapy; wound; neural disorder; nimune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                Human colon cancer antigen nucleotide sequence SEQ ID NO:271.
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BP.
    AAC98261 standard; cDNA; 141
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                                                                                                                                                                                  (first entry)
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Length 141;

100.0%; Score 12; DB 3;

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed aspecification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                 Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 12; DB 4; Length 168; 100.0%; Pred. No. 8.6e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID NO 23318; 639pp + Sequence Listing; English
                                                                                                              Human foetal liver single exon nucleic acid probe #23318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 168 BP; 38 A; 45 C; 37 G; 48 T; 0 U; 0 Other;
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26-MY-2000; 2000US-0207456F.
30-UTN-2000; 2000US-0060408
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-023468TP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000669
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                                                                        (first entry)
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-483447/52.
                                                                                                                                                                                                                                       WO200157277-A2.
                                                                                                                                                                                                  Homo sapiens.
                                                                        01-FEB-2002
                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABS49281;
                                 ABA75013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (1). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the protein sequences in ABB57020 to ABB57374) or by determining the levels or expression profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or therapeuticis for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                               Mouse ischaemic condition related cDNA sequence SEQ ID NO:468
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                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi Y, Nagata T, Ishii Y;
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               Pred. No. 8.6e+03;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 1297; 2690pp; English.
100.08; Pr
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                                                                                                                                                                                                                          ABI99496 standard; cDNA; 151
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                                     12; Conservative
                                                                                                                79 GGAAAGTAAAA 90
                                                                           1 GGAAAGTAAAAA 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-034733/04.
                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-NOV-2001
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                                                                                                                                                                                                                                                                  ABI99496;
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                                     Matches
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ABI99496
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WO200157273-A2

ABA75013 standard; DNA; 168 BP.

RESULT 12 ABA75013/c ID ABA750

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Homo sapiens.

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thale cress; gene; ds; genetic manipulation; plant; biosynthesis; genetic modification; environmental stress; disease resistance; fungicide; insecticide; stress tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 12; DB 5; Length 177; 100.0%; Pred. No. 8.6e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 177 BP; 41 A; 37 C; 42 G; 48 T; 0 U; 9 Other;
                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana polynucleotide #220.
                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1191; 11750pp; English.
                                                                                                                                                         Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-2001; 2001US-00924035.
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11-AUG-2000; 2000US-00638258.
25-MAY-2000; 2000US-0207454P.
09-UUN-2000; 2000US-0211314P.
18-UUL-2000; 2000US-029007P.
13-DEC-2000; 2000US-0255281P.
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1es 12; Conservative
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HARGISS T R.
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                                                                                                                                                                                               WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002142319-A1.
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(HARG/)
(YUYY/)
(RAME/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia whyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at Etp. wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 168 BP; 38 A; 45 C; 37 G; 48 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 7359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 24271; 658pp; English.
                                                                                                                                                                                                                                                                                                                                        Penn SG, Hanzel DK, Chen W, Rank DR
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                                                                                                               04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00609408
03-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-0032459P.
                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0189862P.
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                                                                         30-JAN-2001; 2001WO-US000664
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 GGAAAGTAAAA 151
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RESULT 14

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The invention relates to Arabidopsis thaliana nucleic acid sequences. The DNA sequences and the polypeptides they encode are useful for identifying homologous or related genes, for producing compositions that madulate the expression or function of the polypeptides, for mapping functional captured in diagnosis, for studying associated functional regions of the protein, in diagnosis, for studying associated pathways, for genetic manipulation of cells, preferrably plant cells, in screening assays of various plant strains to determine the strains that are capable of withstanding a particular disease or environmental stress, for enhancing or inhibility production of environmental stress, for enhancing or inhibility production of transgenic organisms, such as plant cells and plants. Transgenic plants are useful for introducing or improving disease resistance and stress to clerance in plants, screening biologically active agents, such as tungicides and insecticides, and for identifying factors involved in biosynthetic pathways of nutritional, commercial or medicinal value. Sequences ABX60655-ABX61554 represent Arabidopsis thaliana
                                                                                                                                                                                                                                                                                            Novel Arabidopsis thaliana nucleic acid useful for constructing a transgenic plant with enhanced disease resistance and enhanced traits of interest, as probes, and in diagnosis and screening purposes.
                                                                                                                                               Gorlach J, An Y, Hamilton CM, Price JL, Hargiss TR, Yu Y;
Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
Garcia CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 77; 277pp; English
                                          LEDFORD B L. WOESSNER J P
                                                                                                                                                                                                                                                    WPI; 2003-102509/09.
                                                                                      HAAS W D.
GARCIA C A.
                                                                (WOES/)
(HAAS/)
(GARC/)
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Search completed: March 25, 2004, 10:25:09 Job time : 16.4532 secs 31 GGAAAGTAAAA 42 qq

1 GGAAAGTAAAA 12

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30519, A 30519, A 100, App 77849, A

Sequence 30519, A Sequence 100, App Sequence 8180, App Sequence 8180, App Sequence 1333, App Sequence 373, App Sequence 373, App Sequence 373, App Sequence 34915, App Sequence 12559, A Sequence 12559, A Sequence 15559, A Sequence 1246, App Sequence 829, App Sequence 1246, App Sequence 1244, App Sequence 1244, App Sequence 1884, A

Sequence 98384, A Sequence 104074, Sequence 155, App Sequence 11484, A Sequence 119129,

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Mark D.
Recombinant Virus Expressing Foreign DNA Encoding
Feline CD80, Feline CD86, Feline CTLA-4 or
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Sequence 123886, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:
APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 318.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2001-01.08

PRIOR APPLICATION NUMBER: 6/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
US-10-085-783A-30519
US-10-242-52A-30519
US-10-082-82BA-30519
US-10-082-82BA-30519
US-10-424-599-77849
US-10-245-53BA-8180
US-10-245-53BA-8180
US-10-245-53BA-8180
US-10-245-539-84822
US-10-424-599-95068
US-10-424-599-34915
US-10-424-599-133130
US-10-424-599-133130
US-10-424-599-13559
US-10-424-599-13559
US-10-424-599-13559
US-10-424-599-11669
US-00-954-531-829
US-00-954-531-829
US-00-954-531-829
US-00-954-531-829
US-10-424-599-105434
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Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-917-800A-155
US-09-960-352-11484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-09-303-040-80/c
j. Sequence 80, Application US/09303040
j. Patent No. US20020051792A1
j. GENERAL INFORMATION:
APPLICANT: Winslow, Barbara J.
TAPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Virus
TITLE OF INVENTION: Recombinant Virus
TITLE OF INVENTION: Reline CD80, Felin
      12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-123886
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Sequence 271, App
Sequence 271, App
Sequence 472, App
Sequence 16691, A
Sequence 16691, A
Sequence 3051, A
Sequence 30575, A
Sequence 30575, A
Sequence 220, App
Sequence 2287, A
Sequence 2287, A
Sequence 2287, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 123886,
                                                                                                                March 25, 2004, 10:03:04; Search time 10.395 Seconds (without alignments) 4297.861 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications Nh:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                              4917892
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.08-09-925-299-271
2.08-10-925-299-271
5.08-10-085-783A-16691
2.08-10-242-535A-16691
08-09-864-671-31340
0.08-10-085-783A-30575
5.08-10-242-535A-30575
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US-09-303-040-80
US-09-925-299-271
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US-10-424-599-52857
US-10-029-386-17951
US-10-424-599-75993
                                                                                                                                                                                                                                                                                                                               Notal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             2458946 seqs, 1861504846 residues
                                                                                                                                                                             US-09-963-285-1_COPY_1692_1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      nucleic search, using sw model
                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length; 2000000000
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Match 1
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                                                                                      nucleic
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RESULT 5
US-10-424-599-472/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 12; DB 9; Length 141; 100.0%; Pred. No. 1.2e+04; cive 0; Mismatches 0; Indels
TITLE OF INVENTION: Feline Interferon-gama And Uses Thereof FILE REFERENCE: 54957-B
CURRENT APPLICATION NUMBER: US/09/303,040
CURRENT FILING DATE: 1999-04-30
BARLIER APPLICATION NUMBER: 60/083,870
BARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 80
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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LOCATION: (141)
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LOCATION: (12)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (13)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
                                                                                                                                                                                                                                          ; TYPE: DNA; CRGANISM: FIV PPR downstream primer US-09-303-040-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (14) OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc_feature LOCATION: (25)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 12; Conserv
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US-09-925-299-271
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and Other Molecules Associated With
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 18-213223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 472
LENGTH: 149
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US-09-925-299-271
Sequence 271, Application US/09925299
| Publication No. US20030040617A9
| Publication No. US20030040617A9
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PA102
| CURRENT APPLICATION NUMBER: US/09/925,299
| CURRENT FILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: ECT/US0/05883
| PRIOR PILING DATE: 2000-03-08
| PRIOR PILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1556
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 271
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LOCATION: (1)..(149)
OTHER INFORMATION: unsure at all n locations
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, OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-271
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
LOCATION: (39)
OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
COGATION: (12)
CTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: miso_feature
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ORGANISM: Homo sapiens
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Best Local Similarity
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Matches
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Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: Litew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFRENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT APPLICATION NUMBER: US 60/2028

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: US 60/271,955

NUMBER OF SEQ ID NOS: 58994
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WESULI,
WESULI,
WESULI,
Sequence 16691, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
APPLICANT: Chondrodene Inc.
APPLICANT: Chondrodene Inc.
APPLICANT: Chondrodene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT APPLICATION NUMBER: US 60/212,535A
CURRENT APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-07-12
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                                                                                                         Length 149;
                                                                                                                                                             Indels
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_100426C.1
US-10-424-599-472
                                                                                                       Query Match
100.0%; Score 12; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0;
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SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                    138 GGAAAGTAAAA 127
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Best Local Similarity 100.
Matches 12; Conservative
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US-10-085-783A-16691
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 16691
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APPLICANT: Chen, Wenchieng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica.X.1
CURRENT APPLICATION NUMBER: US (9)/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US (6)/180,312
PRIOR APPLICATION NUMBER: US (6)/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR PRILING DATE: 2000-10-04
PRIOR PAPLICATION NUMBER: US (6)/236,359
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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                                                           Gaps
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38 21(53223) B
CURRENT APPLICATION NUBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 86937
LENGTH: 160
   Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 160;
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Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0;
100.0%; Score 12; DB 15; 100.0%; Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Clone ID: PAT_MRT3847_49514C.1
US-10-424-599-86937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(160)
PERTURE INFORMATION: unsure at all n locations
PEATURE:
                                                           0; Mismatches
                                                                                                                                                                                                                                                                                            US-10-424-599-86937/c
. Sequence 86937, Application US/10424599
. Publication No. US20040031072A1
. GENERAL INFORMATION:
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                        130 GGAAAGTAAAA 141
                                                           12; Conservative
                                                                                                                   1 GGAAAGTAAAA 12
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Query Match
Best Local Similarity
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US-09-864-761-31340/c
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Indels

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APPLICANT: Lidew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPRENCE: 4231/2005
FILE REPRENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR PAPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-28
PRIOR FILING DATE: 2001-07-28
PRIOR FILING DATE: 2001-07-28
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PRIOR FILING DATE: 2001-07-28
PRIOR FILING DATE: 2001-07-28
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DAT
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                         Best Local Similarity 100.0%; Fred. No. 1.2e+04; Matches 12; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.2e+04;
ive 0; Mismatches 0;
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; ORGANISM: Arabidopsis thaliana
US-09-924-035A-220
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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US-10-242-535A-30575
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US-10-085-783A-30575

j Sequence 30575, Application US/10085783A

j Publication No. US20040037841A1

j GENERAL INFORMATION:
 j APPLICAN: Chondroene Inc.
 j APPLICAN: Liew, C.C.
 TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 FILE REPRENCE: 4231/2002
  CURRENT APPLICATION NUMBER: US/10/085,783A
  CURRENT FILING DATE: 2002-02-28
   PRIOR APPLICATION NUMBER: US 60/305,340
  PRIOR PRILING DATE: 2001-07-13
   PRIOR PLILING DATE: 2001-03-12
   PRIOR FILING DATE: 2001-03-12
   PRIOR FILING DATE: 2001-03-28
   NUMBER OF SEQ ID NOS: 58994
  SOFTWARE: PREAFFILING VARIENT: ABELIAL OF SEQ ID NOS: 58994
  SOFTWARE: PREAFFILING DATE: 2001-02-28
   NUMBER OF SEQ ID NOS: 58994
  SOFTWARE: PREAFFILING VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT: ABELIAL VARIENT
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CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
CTHER INFORMATION: NT HIT: D49387.1, EVALUE 5.00e-90
OTHER INFORMATION: SWISSPROT HIT: Q14914, EVALUE 1.00e-26
US-09-864-761-31340
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100.0%; Score 12; DB 9; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
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PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
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ORGANISM: Homo sapiens
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US-10-085-783A-30575
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illarity 100.0%; Pred. No. 1.2e+04;
Conservative 0; Mismatches 0; Indels
RESULT 12
US-09-924-035A-220
| US-09-924-035A-220
| Sequence 220, Application US/09924035A
| Patent No. US20020142319A1
| GENERAL INFORMATION:
| TILLE OF INVENTION: Annual APPLICANT: GTIACh VINDERTION: TILLE OF INVENTION: TABLE REFRENCE: 2011US
| CURRENT APPLICATION NUMBER: US/09/924,035A
| CURRENT PILING DATE: 1999-08-11
| PRIOR FILING DATE: 1999-08-13
| NUMBER OF SEQ ID NOS: 900
| SOFTWARE: ResUSEQ for Windows Version 3.0
| LENGTH: 181
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Length 172;

Score 12;

100.08;

Query Match

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: And Januar
APPLICANT: About Thua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EROGIH: 213
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ORGANISM: Glycine max

FRATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_39636C.1

US-10-424-599-75993
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Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 100.
Matches 12; Conservative
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| Sequence 17951, Application US/10029386
| Publication No. US20030194704A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Penn, David R. APPLICANT: Penn, David R. APPLICANT: Penn, STATE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REPRESENCE: ASOUNCE: 
                                                                                                                                                                                                                           APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ENG ID NO 52857
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 14
OTHER INFORMATION: NT HIT: gil5718688, EVALUE 2.00e-78
OTHER INFORMATION: SWISSPROT HIT: BP908569.1, EVALUE 1.00e-80
US-10-029-386-17951
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100.0%; Score 12; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ), OTHER INFORMATION: Clone ID: PAT_MRT3847_18742C.1
US-10-424-599-52857
                                                                                                                    ; Sequence 52857, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
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US-10-424-599-75993
; Sequence 75993, Application US/10424599
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Best Local Similarity 100.
Matches 12; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Glycine max
                                             RESULT 13
US-10-424-599-52857/c
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Gaps

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Title: Perfect score:

Sequence:

1

OM nucleic

Run on:

Scoring table:

Searched:

Minimum I Maximum I

Database

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Mus musculus (house mouse)

Mus musculus

Eukaryota; Matazoa, Chordata; Craniata; Vertebrata; Buteleostomi;

Mummalia; Butheria; Rodenia; Sciurognathi; Muridae; Murinae; Muss.

1 (bases 1 to 37)

1 (bases 1 to 37)

1 Longacre, S., Mahmoud, M., Mesen, E., Pedersen, T.,

Islam, H., Longacre, S., Mahmoud, M., Mesen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Londact: Robert B. Weiss

University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5006

Fax: 801 585 7177
CC400241 0180561-0
CC099593 6608.1130
CC099593 6608.1130
CC049447 018058-0
EX547641 Arabidops
CC846964 0180554-0
AV832401 AV832401
CC0663748 PUTAH311B
CC0663748 PUTAH311B
CC0466155 0180579-0
CC046155 0180579-0
AL92319 Arabidops
BH078101 RPC1-24-2
BL95080 GÉ1144008-0
AL92319 Arabidops
BH078101 RPC1-24-2
EX29744 BX29744
BX22744 BX297444
BX22744 BX297444
BX22744 BX297444
BX226708-0
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AZ26716 RPC1-24-1
CC048069 0180408-0
AZ268185 RPC1-24-1
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AV354395 AV844395
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AL759355 Arabidops
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CG570474 OST199408
AV354395 AV309354
BX766472 BX766472
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BX766472 BX766472
AX103768 MALTHOUST
BH76214 AV309354
BX766472 BX766472
AX103768 MALTHOUST
BR76311606.5
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2M0212K19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0212K19 F, genomic survey sequence.
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                             BX547641
CG846984
AV8246914
CG063748
CF046155
CF046155
AI509743
AD942319
BH095080
CG466358
BH686302
BUR65302
BUR65302
BUR65302
BUR65302
                                                                                                                                                                                                                           BU833252
AL759355
BI452728
AZ889185
CG570474
AV354395
BM750390
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BI188234
BI191170
AV309354
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CC048069
AZ043161
AU256208
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BZ487651
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GSS.
    AZ949109
    RESULT 1
AZ949109
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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COMMENT
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BQ078148 fy85b01.y
CG427224 01S0726-0
BH850672 SALK_0716
                                                                    March 25, 2004, 09:53:09; Search time 90.6845 Seconds (without alignments) 3951.570 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                               55026578
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                            27513289 segs, 14931090276 residues
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                        US-09-963-285-1_COPY_1692_1703
12
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                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BQ078148
CG427224
BH850672
                                                   nucleic search, using sw model
                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em gas inv: *
em gas yln: *
em gas fun: *
em gas fun: *
em gas mus: *
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em_gas_rod:*
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DB seq length: 200000000
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5

Score

Result No. 2222

H 07 10 4

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Email: zbrafish@watson.wustl.edu
cDNA Library construction by: Joe Barnes and Steve Johnson. DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany
(web address: www.rzpd.de)
Seq primer: T3 ET from Amersham.
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01S0726-07A1-H10 UniformMu MuTAIL Library Zea mays genomic clone 01S0726-07A1-H10, genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo, 14 somite"
/lab.host="DH.OB"
/clone_lib="Zebrafish C32 14 somite embryo"
/none="Vector: pAmpl, Site_1: EcoRI, Site_2: NotI; First
strand cDNA synthesis was primed using oligo-dT on
magnetic beads with an additional primer
5. goggcogcataataggactacta-taggg-3'. Second strand
synthesis was a 3-cycle PCR using the primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Telion of the formulation of the
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Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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Plant Molecular and Cellular Biology Program
University of Florida
University 010690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322

    .65
/organism="Danio rerio"
/mol_type="mRNA"
/strain="C32"

                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:7955"
/clone="IMAGE:5816785"
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Unpublished (2003)
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AUTHORS
TITLE
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CG427224
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G
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
// Jab host="Coli strain XIIO-Gold, TI-resistant, F-"
// Jab host="E. coli strain XIIO-Gold, TI-resistant, F-"
// Jab host="E. coli strain XIIO-Gold, TI-resistant, F-"
// Colome lib="Mouse 10kb plasmid UUGCZM library"
// Note="Vector: PWD4Znv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide Kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarced from a derivative
of pwD42 (gi|4732114|gb|A1229072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: K column: 19
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ078148.1 GI:19907185
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/unitivar="genuic DNA"
/strain="W22 (ACR, bz1-m9)"
/strain="W22 (ACR, bz1-m9)"
/strain="W22 (ACR, bz1-m9)"
/clone="UniformMu"
/db xref="taxon.6457"
/clone lib="UniformMu MuTAIL Library"
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1 (bases 1 to 73)
Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deputation (2003)

Contact: Donald R. McCarty

University of Florida

PO 110690 Gainesville, F. 32611-0690, USA

Tel: 322-392-1928 x322

Email: drm@ufl.edu

Sequence flanking probable Mu insertion site in UniformMu line: 0150561-04, Primer set: A

Class: transposon insertion site.

Location/Qualifiers
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       Length
100.0%; Score 12; DB 28;
100.0%; Pred. No. 3.3e+05;
ive 0; Mismatches 0;
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Triticum aestivum (bread wheat)
Triticum aestivum
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/organism="Zea mays"
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       Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                                                                      BH850672 67 bp DNA linear GSS 13-JUN-2002 SALK 071670.53.75.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_071670.53.75.x, genomic
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/clone="SALK 071670.53.75.x" |
/clone="PLP" | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data | data |
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Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 67)
Alonso, J.W., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexman, J. and Ecker, J.R.
Arabidopsis Genome
Unpublished (2001)
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 538 539
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 12; DB 29;
100.0%; Pred. No. 3.3e+05;
ive 0; Mismatches 0;
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/mol_type="genomic DNA"
/strain="Columbia 0"
                                                      organism="Zea mays"
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Location/Qualifiers
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Triticum.
(bases 1 to 78)
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1 (bases 1 to 81)
Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                             93, Fue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 00
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infoblogen.fr).
                                                                                   Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       population
Unpublished (2003)
Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drawdufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
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/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="recital"
/db_xref="texxon:4565"
/clone="6608113005"
/clssue_type="grain" (608 degrees per day after pollination)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 12; DB 14;
100.0%; Pred. No. 3.1e+05;
ive 0; Mismatches 0;
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/clone="01S-458-3-7to12-G02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /moi_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="G608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:29464338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 12, Conservative
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                                                                         Genoplante.
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GSS.
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CC049447
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Submitted (01-JUL-2003) Weisshaar, B.

Li,Y., Strizhov,N., Rosso,M. and Weisshaar, B.

Direct Submission

Submitted (01-JUL-2003) Weisshaar B., Max-Planck-Institut fuer
Submitted (01-JUL-2003) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene Ari302040. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found ad/GABI-Kat/.

Location/Qualifiers
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="Columbia 0."
/db_xref="taxon:3702"
/dlone="CK-546f08-020630"
/clone="CK-546f08-020630"
/clone="CK-546f08-02063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX547641 GSS 02-JUL-2003 Arabidopsis thaliana T-DNA flanking sequence GK-546F08-020630, genomic survey sequence.
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                                           UniformMu maize population by the thermo assymmetric interlaced PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots,
rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B., A mew Arabidopais thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
insertions in Mu inactive lines were extracted from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 81;
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100.0%; Pred. No. 3e+05;
ive 0; Mismatches 0;
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BX547641.1 GI:32440450
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Best Local Similarity 100.
Matches 12; Conservative
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Beprantophyta, Pageralophyta, Beprantophyta, Dageae, PhCCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 105)
Rehitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="leaves"
/dev stage="vegetative stage"
/clone lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG063748 10-6 1.0 KB Zea mays genomic clone ZMMBTa0537F14,
                                                                                                                             Barley, EST sequencing project in NIG and Okayama Univ Unpublished (2001)
Contact: Kazuhiro Sato
Research Institute for Bioresources
Chayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato, K., Salsho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission;
                                                                                                                                                                                                                                                                                                                                                                          database:http://www.shigen.nig.ac.jp/barley/Barley.html.
Location/Qualifiers
1. 102
/organism="Hordeum vulgare subsp. vulgare"
/mol type="mRNA"
/cultivar="Akashinriki"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 102;
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Pred. No. 2.7e+05;
0; Mismatches 0;
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/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sub_species="vulgare"
/db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2003)
Other GSSs: PUIAH31TD
Contact: Cathy Whitelaw
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Best Local Similarity 100.
Matches 12; Conservative
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JOURNAL
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CG063748
LOCUS
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/organism="Zea mays"
/mol type="Genomic DNA"
/etrain="Wa2 (ACR, bz1-m9)"
/etrain="Wa2 (ACR, bz1-m9)"
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/elone lib="UniformNu MirAIL Library"
/elone lib="ToPO-PCR4; DNA flanking Muransposon
/note="Vector: TOPO-PCR4; DNA flanking Muransposon
/note="Vector: TOPO-PCR4; DNA flanking muranteric
/note="Vector: TOPO-PCR4; DNA flanking muranteric
/note="Vector: TOPO-PCR4; DNA flanking muranteric
/note="Vector: TOPO-PCR4; DNA flanking muranteric
/note="Vector: ToPO-PCR4; DNA flanking primers specific for
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers, Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
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AV832401. GI:14524490
                                                                                                                                                                                                                                                           CG846984 11-NOV-2003 17-NOV-2003 0150554-03C1-CO7 UniformMu MuTAIL Library Zea mays genomic clone 0150554-03C1-CO7, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deputation
Unpublished (2003)
Unpublished (2003)
Contact: Donald R. McCarty
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drm@ull.edu
Sequence flanking probable Mu insertion site in UniformMu line: 0150554-03, Primer set: C
Class: transposon insertion site.
Location/Qualifiers
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Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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                                                    Gaps
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  100.0%; Score 12; DB 29; Length 85; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
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     Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity
Matches 12; Conserv
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DEFINITION
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ORGANISM
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VERSION
KEYWORDS
SOURCE
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AV832401
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AUTHORS
TITLE
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KEYWORDS
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Gaps

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GSS 19-AUG-2003

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Helianthus paradoxus
Helianthus paradoxus
Helianthus paradoxus
Helianthus paradoxus
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Heliantheae; Helianthus.

Eliantheae; Helianthus.

Eliantheae; Helianthus.

Scozik, A., Michelmore R.W., Knapp,S., Matvienko,M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Linttuce and Sunflower ESTs from the Compositae Genome Project
http://comggenomics.ucdavis.edu/
Longublished (2002)
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QHL21J23.yg.abl QH L sunflower H.paradoxus (salt stress) Helianthus paradoxus cDNA clone QHL21J23, mRNA sequence.
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/done_lib="CPL sunflower H.paradoxus (salt stress)"
/note="weetor: pGEM-T; The library was constructed from
four different sources (seedling, root, leaf and flower)
of RNA from a single genotype. CDNAs were pooled and
cloned into a high-copy vector pGEM-T. Details of library
construction can be obtained at http://cgpdb.ucdavis.edu/
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Diversity of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-752-9659
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Fax: 1-(540)-752-969
Fax: 1-(540)-75
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Unpublished (1997)
Contact: Nobert Strausberg, Ph.D.
Emall: cgapbs-r@mall.nih.gov
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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vx23d04.yl Soares_thymus_2NDMT Mus musculus cDNA clone
IMAGE:1265287 5', mRNA sequence.
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100.0%; Pred. No. 2.6e+05;
iive 0; Mismatches 0;
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Location/Qualifiers
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/db_xref="taxon:73304"
/clone="QHL21J23"
                                                                                                                                 CF084097.1 GI:33123140
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AI509743.1 GI:4408648
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AI509743
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(clone="0180579-051-H10"

/clone="1080579-051-H10"

/note="vector: TOPO-PCR4; DNA flanking Mu transposon

Insertions in Mu inactive lines were extracted from the

UniformMu maize population by the thermo assymmetric

interlaced PCR (TAIL) protocol using primers specific for

interlaced PCR (TAIL) protocol using primers specific for

brimers. Amplicons were size enriched using Sepharose 400

spin columns and cloned into the TOPO PCR4 vector."
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
        /db_xref="taxon:4577"
/clone="ZMMBTa0537F14"
/clone="Ib="ZM_0.6_1.0_KB"
/clone_Tib="ZM_0.6_1.0_KB"
/note="Vector: pCR4_TOP0, Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG466155 108 bp DNA linear GSS 26-SEP-20 0180579-09A1-H10 UniformMu MuTAIL Library Zea mays genomic clone 0180579-09A1-H10, genomic survey sequence.
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Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 325-3292-1928 x322
Email: drawaffl.edu
Sequence flanking probable Mu insertion site in UniformMu line: 0150579-09, Primer set: A
Class: transposon insertion site.
Location/Qualifiers
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Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
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/mol type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
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Li, Y., Strizhov, N., Rosso, M. and Weisshaar, B.

Li, Y., Strizhov, N., Rosso, M. and Weisshaar, B.,

Burnetted (21-0CT-2002) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion within the locus defined by clone MSD24. The

sequences are generated at the MPI for Plant Breeding Research in

the context of the GABI-Kat project. GABI-Kat is part of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue trpe="Thymus"
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/dev stage="4 weeks"
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/note="Vector: pT7T3D-Pac"(Pharmacia) with a modified
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/mas primed with a Not I - oligo(dT) primer [5'
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/mas primed with a Not I - oligo(dT) primer [5'
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/mas primed with a Not I - oligo(dT) primer [5'
/mas primed with a Not I - oligo(dT) primer [5'
/mas primed with a Not I - olig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3/]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana T-DNA flanking sequence GK-265All-014998, Alabidopsis urvey sequence.
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                                                                                This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the correct orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
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100.0%; Pred. No. 2.6e+05;
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                                                                                                                                                                                                                   Seg primer: -40RP from Gibco.
Location/Qualifiers
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
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Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/. Location/Qualifiers
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1M0276015F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0276015 F, genomic survey sequence.
A2465994
GSS.
                                                        AA330856 v271C06.s
AD255210 AU255210
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BH864357 SALK 0958
CC888324 SALK 1516
AL764318 Arabidops
AU255936 AU255936
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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CC795092
AU103894
BH911549
BH911549
BH861183
AZ307595
AZ865355
BH861183
AZ777486
AZ606694
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AU257598
BH864657
AU254247
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AZ417527
BZ290162
AA600618
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Mus musculus
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Tel: 801 585 5606
Fax: 801 585 7177
   RESULT 1
AZ465994/c
LOCUS
DEFINITION
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ORGANISM
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AZ481958 1M0306G07
AZ663647 1M0543G20
AL479789 T. brucei
                                                                                                      March 25, 2004, 09:53:09; Search time 68.0134 Seconds (without alignments) 3951.570 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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AZ481958
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                                                                                                                                                                   US-09-963-285-1_COPY_223_231
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Maximum Match 100%
Listing first 45 summaries
                                                                        nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_estbum.*
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Perfect score:
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                                                                            OM nucleic
                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                     Seguence:
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                                                                                                         Run on:
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FEATURES

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/Bab. mail.
/ Jab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/ clone lib="Mouse 10kb plasmid UUGCIM library"
/ note=""Vector: PMD42nv; Purifited genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dhares/). The DNA
was blydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gfrom a derivative
cf pWD42 (gi|4732114|gpl,AF129072.1), a copy-number
inducible derivative of plasmid Al. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 24)
Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                              Insert Length: 10000 Std Error: 0 Plate: 0306 row: G column: 07 Seg primer: CACACAGGAAACAGCTATGACC Class: plasmid ends ends: plasmid ends stop: 24. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
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Fax: 801 585 7177
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84112, USA
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AUTHORS
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AZ663647
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note=="WeatOr: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (documents/dnares/). The DNA
was hydrodynamically sheared by repated edpassage through a
0.005 inch orifica at constant velocity. The sheared DNA
was hydrodynamically sheared by reported excess. The
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gi|4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Weiss Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Mus musculus
Bukarusculus
Bukarusculus
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases I to 24)
Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0276 row: O column: 15
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0276015"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="Male"
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Fax: 801 585 7177
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Best Local Similarity
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AZ481958/c
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/clone="SALK 095812"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
insert libraries for whole genome shotgun sequencing projects. In deannes Sequencing, A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. bruce; sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
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Pred. No. 1.7e+05;
0; Mismatches 0;
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/mol type="genomic DNA"
/strain="TREU927"
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/clone="212f07"
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100.0%; Pred. No.
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/strain="Columbia 0"

    .26
    organism="Arabidopsis"

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BH864357.1 GI:22100255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil 4732114 (gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
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1 (bases 1 to 25)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N.,

Dialy, S. B., Bajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CBIO 1SA, B-mail: barrell@sanger.ac.uk and

hl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
/lab host="B. Coli strain Xillo-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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T. brucei sheared genomic DNA clone 212f07, forward sequence,
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Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae,
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   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0543 row: G column: 20
Seq primer: GGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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                                                                                                                                                                                                                                                                 1. .24 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0543G20"
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/organism="Arabidopsis thaliana"
/wol_type="genomic DNA"
/strain="Columbia 0"
/strain="Columbia 0"
/db xref="toxon:3702"
/dlone="GK-124006-012813"
/clone="Ib="Arabidopsis thaliana T-DNA insertion lines"
/clone="Ib="Arabidopsis thaliana T-DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC16! The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                        Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene Al1970560. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 bp mRNA linear EST 25-APR-2002
AU255936 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0006850 3', mRNA sequence.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                     Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                              Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                        A pipeline for automated high-throughput generation of Fk
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
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Kato,K. and Marcba,R.
Generation of expressed sequence tags from mouse brain Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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AU255936.1 GI:20319148
                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 31)
                                                                                                            and Weisshaar, B.
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Arabidopsis thaliana T-DNA flanking sequence GK-124C06-012813,
genomic survey sequence.
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                                                                                                                                                                                                              CC888324 151694.27.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana Genomic clone SALK_151694.27.60.x, genomic Arabidopsis thaliana genomic clone SALK_151694.27.60.x, genomic
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| clone="SALK 151694.27.60.x" |
| clone="SALK 151694.27.60.x" |
| clone="lib="Arabidopsis thaliana TDNA insertion lines" |
| note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 26)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is single pass sequence recovered from the left border of
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis Genome divisity of insertion mutations in Arabidopsis Genome (2001)
Contact: Joseph R. Ecker
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 558 6379
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 9; DB 29; Length 26; 100.0%; Pred. No. 1.7e+05; ive 0; Mismatches 0; Indels
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/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDNA tagged.
Location/Qualifiers
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CC888324
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/clone_lib="3'-directed mouse cDNA library"
                                                                                                                                                                                                       100.0%; Score 9; DB 9; Length 34; 100.0%; Pred. No. 1.7e+05;
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Arabidopsis thaliana (thale cress)
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/db_xref="taxon:10090"
/clone="BED0004806"
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Mus musculus
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34 bp mRNA linear EST 23-APR-1998 vz71c06.s1 Scares_mammary_gland_ubbwg wu weculus cDNA clone T.T.AAGE:1331914 3' similar to SW:UBSC_HUMAN P47986 UBIQUITIN-CONJUGATING ENZYME E2-17 \( \frac{KD}{KD} \) ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
Marra, M.; Hillier, L., Allen, M.; Bowles, M.; Dietrich, N.; Dubuque, T.;
Geisel, S.; Kucaba, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.;
Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.;
Theising, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HMI Mouse BST Project
Unpublished (1996)
Contact: Marraw M/Mouse BST Project
WashU-HHMI Mouse BST Project
WashU-HHMI Mouse BST Project
WashU-HHMI Mouse BST Project
WashIngton University School of MedicineP
4444 Proset Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Soares mammary gland NDMMG"
/note="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                 Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                               100.0%; Score 9; DB 9; Length 33; 100.0%; Pred. No. 1.7e+05; Live 0; Mismatches 0; Indels.
8916-5 Takayama, Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: ktato@bs.aist-nara.ac.jp,
URL:http://lovez.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="IMAGE:1331914"
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BES97035 SALK_099290.19.00.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_099290.19.00.n, genomic
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAP2 (gil 4/732114/194)AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                 /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G79EL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 9; DB 28; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: H column: 02
Seg primer: CACACAGGAAACAGCTATGACC
Class: pleamid ends
High quality sequence stop: 37.
Location/Qualifiers
                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0103H02"
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AZ401018.1 GI:10516092
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Fax: 801 585 7177
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                          Eukaryota; Viridiantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 34)
S Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 858 4379
Email: ecker@salk.edu
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2M0103H02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0103H02 R, genomic survey sequence.
AZ827214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="taxon:3702"
/clone="SALK 099290.19.00.n"
/clone="SALK 099290.19.00.n"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 37)
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 1005, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duni, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Tokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is single pass sequence recovered from the left border of
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/organism="Arabidopsis thaliana"
/wol_type="genomic DNA"
/srrain="Columbia 0"
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9, Conservative
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Fax: 801 585 7177
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AZ827214/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.001d (Stratagene) cells and selected for ampicillin resistance."
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyra; Magnoliophyra; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab.host="E. Coli strain XLIO-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"
/note=""Vector: PWD42rv, Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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100.0%; Score 9; DB 28; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seg primer: CGTTGTAAAACGACGCCAGT
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High quality sequence stop: 41.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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/strain="C57BL/60"
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/clone="UUGC1M0273J07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil 4732114 gb] APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
/lab.host="B. Coli strain XLIO-Gold, TI-resistant, F-"
/lab.host="B. Coli strain XLIO-Gold, TI-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                      Insert Length: 10000 Std Error: 0.00 Plate: 0167 row: K column: 04 Seg primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 40. Location/Qualifiers
                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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/strain="c57BL/60"
/db xref="taxon:10090"
/clone="UUGCIMO167K04"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
    Email: ddunn@genetics.utah.edu
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Mus musculus
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Fax: 801 585 7177
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| crganism="Arabidopsis thaliana" |
| crganism="Arabidopsis thaliana" |
| mol_type="genomic_DNA" |
| strain="Columbia on DNA" |
| strain="Columbia on DNA" |
| strain="Columbia on DNA" |
| clone="taxon:3702" |
| clone="taxo
Direct Submission
Submitted (21-0CT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-0CT-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene At4915370. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mgg.de/GABI-Kat/.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels

1 ACAAATGTT 9

13 ACAAATGTT 21

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Search completed: March 25, 2004, 15:30:04 Job time: 73.0134 secs

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Query Match
100.0%; Score 9; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 25, Appl
Sequence 26, Appl
Sequence 363, Appl
Sequence 36, Appl
Sequence 84, Appl
Sequence 8462, Appl
Sequence 1602, Appl
Sequence 15021, Appl
Sequence 15021, Appl
Sequence 15022, Appl
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Sequence 84, Appl
Sequence 57, Appl
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4297.861 Million cell updates/sec
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                                                                                                                                                                  March 25, 2004, 10:03:04; Search time 7.79622 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-098-263B-15021
US-10-098-263B-15022
US-10-098-263B-16053
US-10-098-263B-16054
US-10-098-263B-228B1
US-10-098-263B-228B1
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US-09-989-643-84
US-09-864-029-57
US-10-114-270-296
US-10-032-585-4249
US-10-130-363
US-10-452-59-8
US-09-969-373-3149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2458946 seqs, 1861504846 residues
                                                                                                                                                                                                                                                                          US-09-963-285-1_COPY_223_231
9
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match
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                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                     Run on:
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263	26	263	26	263	263	263	263	263	263	263B	263	263	263	263	263	263B	263	263	26	263	263	263	263	263	263	26	263	853	55	
60	-860	60	9	60	60	9	9	60	60	9	9	9	9	60	9	60	6	8	9	60	60	60	60	60	60	-860	6	75	-262-	
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ALIGNMENTS

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Sequence 14, Application US/10370860A
PUBLICATION
GENERAL INFORMATION:
APPLICANT:
 NUMBER:
APPLIC
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ORGANISM: Artificial Sequence
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Gaps 0

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APPLICANT: Picard, Francis J.
APPLICANT: Paracis J.
APPLICANT: Paracis J.
APPLICANT: Paracis J.
APPLICANT: Paracis J.
APPLICANT: Pouglette, Marc
APPLICANT: Pouglette, Marc
APPLICANT: Pouglette, Marc
TITLE OF INVENTION: Species Specific, Genus-Specific and Universal DNA
TITLE OF INVENTION: Probes and Amplification Primers to Rapidly Detect and
TITLE OF INVENTION: Associated Antibictic Resistance Genes from
TITLE OF INVENTION: Associated Antibictic Resistance Genes from
TITLE OF INVENTION: ASSOCIATED ANTIBICATION NUMBER: 09/297,539
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/297,539
PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-09
PRIOR FILING DATE: EARLIER FILING DATE: 1996-11-04
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 84
LENGTH: 22
LENGTH: 22
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APPLICANT: Casman, Stacie J.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gasman, Stacie J.
APPLICANT: Gasman, Stacie J.
APPLICANT: MacDougall, John R.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Since, David J.
APPLICANT: Solution and J.
APPLICANT: David J.
APPLICAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Majumder, Kumd
APPLICANT: Tchernev, Velizar T.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Szekeres Jr., Edward S.
APPLICANT: Alsobrook II, John P.
APPLICANT: Burgess, Catherine E.
APPLICANT: Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                          ; Sequence 84, Application US/09989643
; Publication No. US20030049636A1
; GENERAL INFORMATION:
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Publication No. US20030082174A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
1 ACAAATGTT 9
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US20040030110Alel Proteins and Nucleic Acids Encoding Same
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Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: , OTHER INFORMATION: oligonucleotide primer US-09-864-029-7
PRIOR FILING DATE: 2000-07-19
FROR APPLICATION NUMBER: 60/207,020
FRIOR APPLICATION NUMBER: 60/207,020
FRIOR APPLICATION NUMBER: 60/207,020
FRIOR APPLICATION NUMBER: 60/239,542
FRIOR APPLICATION NUMBER: 60/239,542
FRIOR FILING DATE: 2000-07-25
FRIOR PELING DATE: 2000-10-10
FRIOR FILING DATE: 2000-12-18
FRIOR APPLICATION NUMBER: 60/274,645
FRIOR APPLICATION NUMBER: 60/274,645
FRIOR APPLICATION NUMBER: 60/274,645
FRIOR FILING DATE: 2001-02-66
FRIOR FILING DATE: 2001-03-09
FRIOR FILING DATE: 2001-03-09
FRIOR FILING DATE: 2001-03-09
FRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 296,.Application US/10114270 Publication No. US20040030110A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li, Li
Vernet, Corine
Zerhusen, Bryan D.
Gorman, Linda
Shenoy, Suresh G.
Pena, Carol B.A.
Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MacDougall, John R
Rothenberg, Mark E
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Gusev, Vladimir Y
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FILE REFERENCE: 21402-322C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stone, David J
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APPLICANT: Taupier, Raymond J., Jr.
APPLICANT: Taupier, Raymond J., Jr.
APPLICANT: Taupier, Raymond J., Jr.
APPLICANT: Saterian, Elina
APPLICANT: Shenoy, Suresh G.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-416C (Cura-716 SMT)
CURRENT FALING DATE: 2002-68-01
PRIOR APPLICATION NUMBER: 60/30,501
PRIOR APPLICATION NUMBER: 60/316,508
PRIOR APPLICATION NUMBER: 60/316,508
PRIOR PLING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR PLING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,991
PRIOR APPLICATION NUMBER: 60/310,991
PRIOR PLING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,991
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/313,936
PRIOR PLING DATE: 2001-08-05
PRIOR PLING DATE: 2001-08-05
PRIOR PLING DATE: 2001-08-05
PRIOR PLING DATE: 2001-08-05
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 369
   Sequence 363, Application US/10210130 Publication No. US20040014053A1
                                                                                                                                                                                                                                                                                                                                     bergha, Constance
Bergha, Mei
Casman, Stacie J.
Voss, Edward Z.
Boldog, Ferenc L.
Padigaru, Muralidhara
Smithson, Glennda
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Vernet, Corine A.M.
Leite, Marlo W.
Guo, Xiaojia Sasha
Anderson, David W.
Spytek, Kimberly A.
Gerlach, Valerie
Burgess, Catherine E.
Khramtsov, Nikolai V.
                                                                                          APPLICANT: Zerhusen, Bryan D.
APPLICANT: Patturajan, Meera
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Rieger, Daniel K.
APPLICANT: Pena, Carol E.A.
APPLICANT: Shinkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ort, Tatiana
Ellerman, Karen
Rastelli, Luca
Agee, Michele L.
Chaudhuri, Amitabha
Chant, John S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DiPippo, Vincent A. Edinger, Shlomit R. Eisen, Andrew J. Gangolli, Esha A.
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Ooi, Chean Eng
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US-10-032-585-4249/c
is Sept-4249, Application US/10032585
is Publication No. US20030180953A1
is Publication No. US20030180953A1
is GENERAL INFORMATION:
is APPLICANT: Bo, Jiang
is APPLICANT: Charles, Boone
is APPLICANT: Howard, Bussey
if TILE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
if TILE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
if TILE REFERENCE: 10182-005-999
if CURRENT FILING DATE: 2001-12-20
is NUMBER OF SEQ ID NOS: 8000
is SOFTWARE: ParentIn version 3.1
is SEQ ID NO 4249
il ENGTH: 23
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                           CURRENT FILING DATE: 2002-11-27

PRIOR PAPLICATION NUMBER: 60/281,086

PRIOR FILING DATE: 2001-04-03

PRIOR FILING DATE: 2001-04-03

PRIOR PELICATION NUMBER: 60/281,136

PRIOR PELING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-04-05

PRIOR PILING DATE: 2001-04-05

PRIOR PELING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 60/282,020

PRIOR PILING DATE: 2001-04-10

PRIOR PELING DATE: 2001-04-10

PRIOR PELING DATE: 2001-04-10

PRIOR PELING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 60/283,710

PRIOR PELING DATE: 2001-04-12

PRIOR PELING DATE: 2001-04-13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Score 9; DB 12; I
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/114,270 CURRENT FILING DATE: 2002-11-27
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ORGANISM: Artificial Sequence
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US-10-032-585-4249
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Best Local Similarity
Matches 9; Conserv
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US-10-210-130-363/c
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Length 25;

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Sequence 8462, "Application US/10098263B
FUBLICATION NO. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mitthen) Michael
TITLE OF INVENTION: Human Microarray
FILE REPERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
FRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03.16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 256
LENGTH: 256
LENGTH: 256
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100.0%; Pred. No. 3.7e+04;
rative 0; Mismatches 0; Indels
                                                                                            Query Match 100.0%; Score 9; DB 9; L
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0;
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Best Local Similarity luv...
9; Conservative
                                                                                                                                                                                                                                     14 ACAAATGTT 22
; TYPE: DNA; ORGANISM: Glycine max US-09-969-373-3149
                                                                                                                                                                                           1 ACAAATGTT 9
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; ORGANISM: Homo sapien
US-10-098-263B-15021
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ORGANISM: Homo sapien
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; Publication No. US2004001414A1
; Publication No. US2004001414A1
; GENERAL INFORMATION:
   APPLICANT: MADERN: Mogens Winkel
; APPLICANT: FUCKNING, Marianne Scheel
; TILLE OF INVENTION: Method of Screening for Substances Acting on MSK1
; FILE REFERENCE: 3893-0218P
; CURRENT APPLICATION NUMBER: US/10/452,591
; CURRENT APPLICATION NUMBER: PCT/DX00/00505
; PRIOR FILING DATE: 2003-06-03
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 24
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                         ; OTHER INFORMATION: Description of Artifical Sequence: Primer/Probe US-10-210-130-363
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US-10-452-591-8
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Patent No. US2020133852A1
GENERAL INFORMATION:
APPLICANT: Effetto.
TITLE OF INVANTION: SOPPEAN SSR and Methods of Genotyping
TITLE OF INVANTION: SOPPEAN SSR and Methods of Genotyping
FILE REPRENCE: 38 = 10 (5.5679) A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-05
PRIOR PILING DATE: 2001-01-05
PRIOR PILING DATE: 2001-01-13
PRIOR PILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 3149
                                                                                                                                                                                                          Query Match
100.0%; Score 9; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Score 9; DB 15; L
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0;
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 363
LENGTH: 23
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                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                   23 ACAAATGTT 15
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US-09-969-373-3149
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US-10-452-591-8/c
                                                                                                                     FEATURE:
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Gaps

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Sequence 15021, Application US/10098263B
| Publication No. US20030104410A1 |
| GENERAL INPORMATION: |
| APPLICANT: Mittman Microarray |
| TILLE OF INVENTION: Human Microarray |
| TILLE OF INVENTION: Human Microarray |
| TILLE OF INVENTION: Human Microarray |
| TILLE OF INVENTION: HUMBER: US/10/098,263B |
| CURRENT APPLICATION NUMBER: 60/276,759 |
| PRIOR FILING DATE: 2003-01-08 |
| PRIOR FILING DATE: 2001-03-16 |
| NUMBER OF SEQ ID NOS: 131066 |
| SOFWMARE: Microarray Probe Sequence Listing Generator V 1.1 |
| LENGTH: 25
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100.0%; Score 9; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
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US-10-098-263B-15022
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0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-098-263B-22882
                                                                                                                                              1 ACAAATGTT 9
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      ; ORGANISM: Homo sapien
US-10-098-263B-16054
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ORGANISM: Homo sapien

US-10-098-263B-22881
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US-10-098-263B-22881
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Sequence 16054, Application US/10098263B

Publication No US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REPRENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

FRIOR FYLING DATE: 2001-03

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 16054

LENGTH: 25

TYPE: DNA
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US-10-098-263B-16053/c
| Sequence 16053, Application US/10098263B
| Sequence 16053, Application US/10098263B
| Publication No. US20030104410A1
| GENERAL INFORMATION:
| APPLICAMY: Mittman, Michael
| TITLE OF INVENTON: Human Microarray
| FILE REFERENCE: 310.1
| CURRENT APPLICATION NUMBER: US/10/098,263B
| CURRENT PILING DATE: 2003-01-08
| PRIOR RILING DATE: 2001-03-16
| PRIOR FILING DATE: 2001-03-16
| SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
| SEQ ID NO 16053
| LENGTH: 25
Sequence 15022, Application US/10098263B
Publication No. US2030104410A1
GENERAL INFORMATION:
APPLICANT: Mitchan, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION WUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR PPLICATION NUMBER: 60/276,759
PRIOR PELLING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
LENGTH: 25
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Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapien
US-10-098-263B-16053
                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapien
US-10-098-263B-15022
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; Sequence 22882, Application No. US20030104410A1
; GENERAL INFORMATION:
; AFPLICANT: Mitchael
; TITLE OF INVENTON: Human Microarray
FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 22882
                                                                                                                                                                                                                                                                  Sequence 22881

Sequence 22811, Application US/10098263B

Publication No. US20030104410A1

SEDERAL INFORMATION:

APPLICANT: Mitthenan, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERRENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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100.0%; Score 9; DB 14; Length 25; 100.0%; Pred. No. 3.7e+04; ive 0; Mismatches 0; Indels
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100.0%; Score 9; DB 14; 3
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 9; Conservative 0; Mismatches 0;
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March 25, 2004, 07:40:23 ; Search time 9.33989 Seconds (without alignments) 4093.601 Million cell updates/sec
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GenCore version 5.1.6
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Maximum Match 100%
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1: geneseq11980s:*

2: geneseq11980s:*

4: geneseq12001as:*

5: geneseq12001as:*

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7: geneseq12003as:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abn87945 Human GSR	Aax72750 Mouse flk	Aax72751 Mouse flk	Aav95125 Canine IL	Aav94640 Human IL-	Aav95126 Canine IL	. Aav94639 Human IL-	Aaf04437 Hammerhea	Aaf04884 Hammerhea	Aaf04436 Hammerhea	Aaf04885 Hammerhea	Acc54403 Human tum	Adb42327 Tumour su	Adb44770 Tumour su	Aat91799 Dihydropy	н	Ab189242 HIV-1 rel	Ab189256 HIV-1 rel	Ab189240 HIV-1 rel	Ab189251 HIV-1 rel	Ab189237 HIV-1 rel	Aaa84073 Cyclin C	Aaa84071 Cyclin C
SUMMARIES	DI DI	ABN87945	AAX72750	AAX72751	AAV95125	AAV94640	AAV95126	AAV94639	AAF04437	AAF04884	AAF04436	AAF04885	ACC54403	ADB42327	ADB44770	AAT91799	AAA57101	ABL89242	ABL89256	ABL89240	ABL89251	ABL89237	AAA84073	AAA84071
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PA	(GENA-)	GENAISSANCE	PHARM	INC	Ω.	
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XFF	New genet	etic variants ng efficiency	of	re]	Glutathione reductase isogenes, u 1 reliability in drug development	useful for : for treating
F X	hemolytic	anemia				
PS	Claim 14	4; Page 14;	137pp;		English.	
888	The present reductase (G	invent	des (I).	in in	genetic variants of t	human glutathione and can be used in
381	gene thera	py. (for	ខ្លួ	n a)	in screening for grugs lytic anaemia, Methods f	the present
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diseases associated with GSR activity; for haplotyping, which is also used by the pharmaceutical research scientist to validate GSR as candidate target for treating a specific condition or disease predicted to be associated with GSR activity, e.g. haemolytic anaemia, and in the design of clinical trials for treating a specific condition of disease secondated with GSR activity, e.g. haemolytic anaemia, and in the associated with GSR activity, e.g. haemolytic anaemia, and in the exign of clinical trials for treating a specific condition of disease associated with GSR activity, in screening compounds targeting GSR.

(I) is useful in studying the expression and function of GSR, and in expressing GSR protein for use in screening for candidate drugs to treat diseases related to GSR activity. (I) is also useful in studying the effect of the variation on the biological activity of GSR as well as on the binding affinity of candidate drugs targeting GSR for the treatment of haemolytic anaemia. The present sequence represents an allele specific cligonucleotide (ASO) primer for the human GSR gene, which is given in the month a single nucleotide polymorphic anaemia single nucleotide polymorphism) in the ASO primer is shown using an IUPAC ambiguity code (as given in the present invention)
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AAX72750 standard; RNA; 17 BP
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AAX72750;

Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; MSD; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor; Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #183. 96WO-US017480 95US-0005974P 96US-00584040 (RIBO-) RIBOZYME PHARM INC. (first entry) fms-like tyrosine kinase ; foetal liver kinase 1; ss CHIRON CORP 25-OCT-1996; 26-OCT-1995; 11-JAN-1996; WO9715662-A2 28-JUL-1999 01-MAY-1997. (CHIR) gb.

Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA stability - useful for treating e.g. tumour angiogenesis, psoriasis, rheumatoid arthritis, etc., in a human patient. Claim 4; Page 128; 218pp; English. WPI; 1997-259017/23

Stinchcomb D, Escobedo J;

Pavco P, Mcswiggen J,

The present invention describes nucleic acid molecules which modulate the synthesis, expression and/or stability of a mRNA encoding 1 or more receptors of vascular endothelial growth factor (VBGF). A patient (preferably human) having a condition associated with the level of the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1; KRS; hammerhead ribozyme; hairpin ribozyme; cleavage; tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease; fms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                     þe
fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour anglogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can betreated by administering the nucleic acid molecule or the expression vector to the patient. AAX67275 to AAX75752 represent specific examples of nucleic acid molecules from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stability - useful for treating VEGF receptor(s) gene expression or rheumatoid arthritis, etc., in a human patient.
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No. 3.2e+04;
                                                                                                                                                          100.0%; Score 9; DB 2; Length 17; 100.0%; Pred. No. 3.2e+04; ive 0; Mismatches 0; Indels
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                                                                                                                           Seguence 17 BP; 5 A; 3 C; 4 G; 0 T; 5 U; 0 Other;
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ID AAX72751 standard; RNA; 17
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and AAV93675 to AAV95260 represent specifically claimed ribozymes, and from the present invention. The ribozymes can be used for the treatment of, e.g. graff rejection, autoimmune disease, cancer, psoriasis, allergy and other inflammatory conditions. The ribozymes are also used to induce tolerance in a recipient to alloantigen from a donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer, autoimmune disease and allergies.
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hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
autoimmune disease; psoriasis; allergy; inflammatory disease;
                Human, IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
autoimmune disease; psoriasis; allergy; inflammatory disease;
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AAV95126/c
ID AAV95126 standard; RNA; 17 BP.
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                                                                                         graft rejection, ss
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                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - useful for treating e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain; hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer; autoimmune disease; psoriasis; allergy; inflammatory disease;
Gaps
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  Mismatches
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AAV95125 standard; RNA; 17 BP.
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                                                                                         11 ACAAATGTT
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AAV94640/
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and other inflammatory conditions. The ribozymes are also used to induce tolerance in a recipient to alloantigen from a donor
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                                                                                                                                                                                                            AAF04437 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                      AAF04437;
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                                                                                                                                             The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (II)-2R gamma encoded RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and AAV94575 to AAV95260 represent specifically claimed substrate sequences from the present invention. The ribozymes can be used for the treatment off, e.g. graff rejection, autoimmune disease, cancer, psoriasis, allergy and other inflammatory conditions. The ribozymes are also used to induce tolerance in a recipient to alloantigen from a donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence invention describes ribozymes targeted to modulate the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA. AAV93889 to AAV94574 represent specifically claimed ribozymes, and AAV94575 to AAV95260 represent specifically claimed substrate sequences from the present invention. The ribozymes can be used for the treatment of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer, autoimmune disease and allergies.
                                                                                Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer, autoimmune disease and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain; hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer; autoimmune disease; psoriasis; allergy; inflammatory disease; graft rejection; ss.
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                                                                                                                                                                                                                                                                 Sequence 17 BP; 5 A; 3 C; 3 G; 0 T; 6 U; 0 Other;
                                                                                                                      Claim 4; Page 46; 61pp; English.
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AAV94639 standard; RNA; 17 BP.
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                               Stinchcomb DT, Mcswiggen JA;
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    (RIBO-) RIBOZYME PHARM INC
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hes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                          Length 17;
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Sequence 17 BP; 4 A; 4 C; 2 G; 0 T; 7 U; 0 Other;
                                                   100.0%; Score 9; DB 2; Li
100.0%; Pred. No. 3.2e+04;
tive 0; Mismatches 0;
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AAF04884/C
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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, BRA3/COUP-TF-1. the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoletin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TRZ Orphan receptor, EAR3/COUP-TF-1, the GRAT transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and
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                                                                                             Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                       Mcswiggen J;
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                                                                                                                                                         Claim 4; Page 100; 164pp; English.
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                                      Pavco P,
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            (RIBO-) RIBOZYME PHARM INC
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                                         Zwick M,
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                                         Blatt L,
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                                                                                                                                                                                                                                                                                                                                                           Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
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                                                                                    Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.
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                                                          Hammerhead ribozyme substrate #2400.
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Best Local Similarity
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   AAF04884;
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The invention relates to the isolation of 6327 nucleotide sequences, fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the nucleotides, remained and/or amplifying nucleic acids, as in vitro identifying, quantifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies (Ab) against the polypeptide are useful for prevention and/or treatment of viral infections or diseases characterized by development of tumours or cital degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and/or prognosis of these diseases. The nucleotides and polypeptides can also be used to screen for their specific interactive molecules, potentially useful for treating diseases associated with abnormal expression of the nucleotides associated with abnormal
                                                                                                                                                                              cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
primer; probe; tumour suppression; tumour reversion; apoptosis;
virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 9; DB 9; Length 17; 100.0%; Pred. No. 3.2e+04;
                                                                                                                                 Jumour suppression/reversion associated nucleotide #2650.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 341; 771pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB44770 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR ENGINES LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-2002; 2002WO-IB004219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-2001; 2001FR-00011981.
                                                                     (revised)
(first entry)
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Best Local Similarity luv...
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                       WO2003040369-A2.
                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                     18-DEC-2003
04-DEC-2003
                                                                                                                                                                                                                                                                diagnosis.
                           ADB42327;
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AC ADB44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
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                                                                                                                                           100.0%; Score 9; DB 3; Length 17; 100.0%; Pred. No. 3.2e+04; ative 0; Mismatches 0; Indels
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                                                                                                 Sequence 17 BP; 5 A; 3 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumour suppressor sequence #3170,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuijnder M, Telerman A, Amson R;
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ADB42327
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fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, a sequence that hybridizes under stringent conditions with the nucleotides, or the complement, or corresponding RNA, of the charmalitying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour cuppression or reversion, apoptosis and or viral resistance, to produce recombinant polypeptides, and to prepare transgenic animals, as recombinant polypeptides and or viral resistance, to produce recombinant polypeptides and to prepare transgenic animals, as a containing the vectors. The nucleotides (also vectors containing them and calls containing the vectors), the encoded polypeptides and antibodies of twal infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis and bothors mally useful for treating diseases associated with abnormal
                                                                    cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss; primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
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                                Tumour suppression/reversion associated nucleotide #5093.
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Dihydropyrimidine dehydrogenase genomic fragment PCR primer DPD15.

(first entry)

14-APR-1998

AAT91799

ВР.

AAT91799 standard; DNA; 18

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                                                                                                                                                                                                                                                                                                                                                             Detecting a splicing defect in the di:hydro:pyrimidine dehydrogenase gene - used to identify subjects sensitive to 5-fluorouracil, toxic to individuals with DPD defects.
Human, dihydropyrimidine dehydrogenase, DPD, slicing defect, detection;
5-fluorouracil, cancer, anticancer, uraciluria, PCR primer, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnose DPD-deficiency disorders such as uraciluria
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Copyright (c) 1993 - 2004 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Direct Submission
Submitted (05-NOV-1998) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-MAR-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (11-JUN-1998) Department Of Chemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-AUG-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-OCT-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-OCT-1998) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-OCT-1998) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            Submitted (09-SEP-1997) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                      Direct Submission
Submitted (18-FEB-1998) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                        Direct Submission Submitted (11.MAR-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (17-APR-1998) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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                                                                                                                                                                                                                  (bases 1 to 39961)
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12 (bases 1 to 39961)
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Homo sapiens Chromosome 22q13 Cosmid Clone p76e10, complete
                                                                                                                                                                                                                                                                                                                                                                                                   annotated as STSS were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

Location/Qualifiers
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Fransson, I. and Dumanski, J.P. A cosmid clone in meningioma deletion region of 22q13
structure of variation in the laboratory mouse genome (6915), 574-578 (2002)
                                                                                                                   Whitehead Institute for Biomedical Research, Center for Genome Research
320 Charles Street, Cambridge, MA 02141, USA
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Pan, H., Lin, S. and Roe, B.A.
A cosmid clone in meningioma deletion region of 22q13
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/strain="CZECHII/Ei"
/db_xref="taxon:10090"
/map="+ 16 27-755 66714317-66715044"
/clone lib="CZECHII/Ei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 17; DB 11;
100.0%; Pred. No. 5.8e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
                                                                                                         Contact: Kerstin Lindblad-Toh
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Roe, B.A.
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Transson,I. and Dumanski,J.P.
Unpublished
2 (bases 1 to 43738)
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Submitted (19-SEP-1997) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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Submitted (18-FEB-1998) Department Of Chemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (25-AUG-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Submitted (28-MAR-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
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10 (bases 1 to 43738)
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Submitted (30-OCT-1998) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                Pan,H., Lin,S. and Roe,B.A.
Homo sapiens Cosmid Clone 11119a4 In Meningioma Deletion Region
Unpublished
                                                                                                                                                      AC000034 43738 bp DNA
Homo sapiens Chromosome 22q13 Cosmid Clone
Deletion Region, complete sequence.
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                    TGTGGAAGGAATAAATA 17
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Direct Submission
Submitted (21-JAN-1999) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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                    Submitted (13-NOV-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                 Submitted (16-JAN-1999) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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The University of Oklahoma, 620 Parrington Cval, Room 208, Norman,
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Submitted (01-JUN-2000) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
24 (bases 1 to 39961)
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ON Aug 25, 2002 this sequence version replaced gi:4581185.
Because these overlapping clones came from different libraries.
Location/Qualifiers
1. .39961
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/db_xref="taxon:9606"
/chromosome="22"
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Direct Submission
Submitted (09-APR-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Direct Submission
Submitted (01-SEP-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
19 (bases 1 to 43738)
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Direct Submission
Submitted (13-ARR-1999) Department Of Chemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Direct Submission
Submitted (01-JUN-2000) Department Of Chemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                Direct Submission
Submitted (05-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                  Submitted (12-NOV-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                   Direct Submission
Submitted (13-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-JAN-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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ON Sep 1, 2002 this sequence version replaced gi:4582474.

Because these overlapping clones came from different libraries.

Location/Qualifiers

1. 43738
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Direct Submission
Submitted (30-MAR-2002) Department of Genetics, Washington
University, 444 Porest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 24, 2002 this sequence version replaced gi:19424675.
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Submitted (07-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 44532)
Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases I to 44532)

Sulston, J. E. and Waterston, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                      AC109830 44532 bp DNA linear PRI 30-MP
Homo sapiens BAC clone RP11-1226B8 from 4, complete sequence.
AC109830
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Center code: WUGSC
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Scott, K. and Haglund, K.
The sequence of Homo sapiens BAC clone RP11-1226B8
Upublished (2001)
3 (bases 1 to 44532)
Waterston, R.H.
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Waterston, R.H.
Direct Submission
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

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MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John

1 TGTGGAAGGAATAATA 17 Query Match
Best Local Similarity 100.0

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Gaps

; 0

0; Indels

0; Mismatches

100.0%; Score 17; DB 9; Length 43738; 100.0%; Pred. No. 3.2e+02;

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PRI 28-DEC-2001
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McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                          SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tatemo, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5::1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC015631, 2000 bp overlap; the clone sequenced to the right is RP11-400D2, 2000 bp overlap.
Actual end is at base position 85524 of RP11-400D2.
Location/Qualifiers
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/rpt_family="MaLR"
1418, ,464P
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1418. 4648
/rpt_family="MIR"
3322. 5350
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/rpt_family="AT_riv
5400. .5483
-rpt_family="MIR"
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8954. .19004
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/rpt_family="L1"
9538. . o = ?
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18096. 1812-
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rpt_family="MIR"
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/rpt_family="L2"
5884. .6983
/rpt_family="L1"
7909. .7936
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1820. 1930.
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rpt family="Alu"
2758. .12888
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family="L1"
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Only the 90.5 kb of the T7 end of this project is being submitted.
The remainder overlaps AC005697 [WICGR project L418].
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-11 Human Male BAC"
complement (463. .760)
/rpt_family="Alusg"
complement (875. .1099)
/rpt_family="MIR"
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complement(12099, .12100)
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ement(11451)
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family="AluJb"
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/rpt family="MIR"
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125. .7571
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complement(8134. .8224)
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__.2808
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_.370£
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somplement(5121..5212)
/rpt_family="MIR"
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complement (7572. .7862)
rpt_family="AluJb"
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Center project name: L12518
Center clone name: 218_F_4
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837._.6972
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family="LIME3"
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rpt_family="MIR3"
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complement (2398.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 90843)
                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 90543)
   Homo sapiens chromosome 17, clone RP11-218F4, complete sequence.
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                     Birren B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens chromosome 17, clone RP11-218F4
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Web site: http://www-seq.wi.mit.edu
                                                               AC090287.9 GI:17985917
                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 90543)
                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                  Inpublished
                               ACCESSION
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KEYWORDS
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Consensus quality: 83951 bases at least Q40
Consensus quality: 91885 bases at least Q30
Consensus quality: 93406 bases at least Q30
Consensus quality: 93406 bases at least Q30
Consensus quality: 93406 bases at least Q20
Estimated insert size: 128000; agarose-fp estimation
Batimated insert size: 128000; agarose-fp estimation
Quality coverage: 10.11 in Q20 bases; sum-of-contigs estimation
Quality coverage: 10.24 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
consists of 25 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* trus of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                             Direct Submission
Submitted (15-JUL-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases 1 to 10116)
DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5: contig of 1295 bp in length
5: gap of unknown length
2: gap of unknown length
6: contig of 1077 bp in length
6: contig of 1086 bp in length
7: contig of 1321 bp in length
8: gap of unknown length
8: gap of unknown length
7: contig of 1321 bp in length
7: contig of 1321 bp in length
7: contig of 1893 bp in length
7: contig of 1804 bp in length
7: contig of 1807 bp in length
7: gap of unknown length
7: gap of unknown length
8: gap of unknown length
9: gap of unknown length
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Center clone name: RPCI-23_77J9
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complement(19291. 19390)
/rpt family="WER63"
complement(20076. 20167)
/rpt family="MR3"
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18391. .18395
/notes='<30 qual SNGL region."
complement (18869. .19290)
/rpt family='MLTIA2"
18965. .18977
                                                                                                                                                                                                                                                                                    |15735, .16044
|rpt family="AluJb"
|complement(15892, .15899)
|note="<30 qual SNGL region."
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notce="<30 qual SNGL region."
7837. .17887
rpt_family="AluYb8"
7874. .17939
                                                                     / complement (12482. 12557)
/ rpt family="MER103"
complement (12558. 12820)
/ rpt family="Alux"
complement (12821. 12924)
/ rpt_family="MER103"
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7745. 11775.
                                     ement (12134. .12212)
family="FLAM"
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complement(18030..18868)
rpt_family="MER63"
8236..18242
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rpt_family="Charlie4a"
                      /rpt_family="(ATTTG)n"
complement(12134. .122
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ACO74171.1 GI:9211281
HTG: HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
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5735. .1601
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rpt family="MLT1L"
omplement(17581. .1
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                                                                                                                                                                                                                                                                                                                                                                                                                family="MLT1L"
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15341
/rpt_family="L2"
5507, 1577
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20605. .20915
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FEATURES

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gene="dJ1007G16.4"
fnote="dJ1007G16.4 (heat shock 60kD protein 1 (chaperonin)
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match: proteins: Tr:096783 Sw:002649 Tr:Q9VMN5 Tr:Q9VZ31
Sw:P50140 Tr:064219 Tr:Q9USL7 Sw:P19256 Sw:P18687
Sw:P10905 Tr:Q9USN2 Sw:P35480 Sw:Q3298 Tr:Q9XX77
Sw:P29185 Sw:Q05046 Sw:P20110 Tr:Q95025 Sw:
                                Roswell
further
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.5534. .21667
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note="LiPA2 repeat: matches 4. .6144 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24369. .24451
/note="L2 repeat: matches 2100. .2181 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 72. .193 of consensus"
12525
/note="MIT1H repeat: matches 35. .318 of consensus"
2997. _13700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2748 of consensus"
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note="L2 repeat: matches 2616. ,2739 of consensus"
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13700, .13829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .214. .1379
'note="L2 repeat: matches 1353. .1525 of consensus"
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//note="WIR repeat: matches 51. .203 of consensus"
4304. 4408
//note="L2 repeat: matches 2625. .2748 of consensus
4433. .4570
//note="WIR repeat: matches 91. .222 of consensus"
5459. .5597
//note="L2 repeat: matches 2577. .2710 of consensus
6579. .6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1602. .1740
Thote="MIR repeat: matches 27. .183 of consensus"
2067. .2200
Mir repeat: matches 14. .155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 69. .197 of consensus"
[5414. .15533
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4369. .24451
http://www.sanger.ac.uk/HGP/Chr1
RP5-1007G16 is from the library RPCI-5 constructed at the last Cancer Institute by the group of Pieter de Jong. For Getails see http://bacpac.med.buffalo.edu/
                                                                                                                                     This sequence is the entire insert of clone RP5-1007G16.
Location/Qualifiers
1. .130604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411. .1493
note="L1MC4 repeat: matches 7894. .7977 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note≈"11 copies 2 mer aa 100% conserved"
1653. ,7772
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21737. .23024
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .965 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2822. .2881
//note=="L2 repeat: matches 2655.
complement(3188. .3624)
/note="match: GSS: Em:AQ235526"
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                                                                                                                                                                                                                                                                                                                               /map="p34.2-35.3"
/clone="RE5-1007G16"
/clone lib="RPC1-5"
64. 647
/note="L2_repeat: matches 373.
                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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On Jul 24, 2000 this sequence version replaced gi:9188410.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a not cof the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence, is ambiguous, there is an annotation using the 'unsure'
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Hbuman DNA sequence from clone RP5-1007G16 on chromosome
1p34.2-35.3. Contains part of the gene for a novel CUB and Sushi
(SCR repeat) domain protein, a novel high-mobility group
(nonhistone chromosomal) protein 2 (HMG2) like protein (pseudo)
gene, a heat shock 60kp protein 1 (chaperonin) (HSPD1) pseudogene,
ESTS, STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130604)
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  55414: gap of unknown length
6415 64886: contig of 9072 bp in length
64286: gap of unknown length
70766: contig of 6180 bp in length
70767: 70866: gap of unknown length
7077: 76678: gap of unknown length
7078: gap of unknown length
708: gap of unknown length
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HTG; chaperonin, CUB; HWG2; HSP60; HSPD1; Sushi.
HOmo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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/clone_lib="RPCI mouse BAC library 23"
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RESULT 7

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PRI 12-JUL-2002

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DOE Joint Genome Institute.

Direct Submission

Submitted (03-MG-1999) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Genome Institute and Stanford Human Genome Center.

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submitted (29-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

(Dasses I to 13531)

Control Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1. (bases 1 to 135331)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission

Submitted (12-701-2002) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, A5 94598, USA

On Jul 12, 2002 this sequence version replaced gi:21240680,

Parft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www-shgc.stanford.edu
wdw-shgc.stanford.edu
duality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Quality >=60 Broots is 0.1.
NOTE: This insert is not the entire sequence of the clone. It is clipped at the overlap with AC008507. The number of bases overlapped is 46781.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC008798 135331.bp DNA linear PRI 12-JUL-
Homo sapiens chromosome 19 clone CTD-2057D4, complete sequence.
AC008798
                                                                             38796. .39003

Joote="WARS8A repeat: matches 1. .223 of consensus"

Joote="L2 repeat: matches 2699. .2748 of consensus"

Joote="L2 repeat: matches 2386. .2693 of consensus"

Joote="L2 repeat: matches 1286. .259 of consensus"

Johnte-"MIR repeat: matches 12. .259 of consensus"

Joote="MIR repeat: matches 48. .137 of consensus"

Joote="MIR repeat: matches 48. .137 of consensus"
                           /note="L2 repeat: matches 2288. .2675 of consensus" 38796. .39003
       note="MIR repeat: matches 3. .118 of consensus"
                                                                                                                                                                                                                                                                                                                                     Length 130604;
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100.0%; Pred. No. 2.7e+02;
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/chromosome="19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97118 TGTGGAAGGAATAAATA 97134
                                                                                                                                                                                                                                                                                                                                                                                    0;
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Homo sapiens
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AC008798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               match: profeins: Tr:060494 Tr:Q9TU53 Sw.P13497 Tr:Q9Z135 Tr:043897 Tr:Q9Y561 Sw:P98069 Tr:Q9UQ00 Sw:Q15113 Sw:Q61389 Tr:Q44072 Tr:QSY6L7 Tr:057381 Tr:057382 Tr:Q9WVM6 Sw:Q08628 Tr:Q91925 Tr:Q62381"
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5660. .35774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LTR33 repeat: matches 44. .119 of consensus" 9715. .30122 note="LTR33 repeat: matches 102. .517 of consensus" 10214. .30320 repeat: matches 2. .102 of consensus" 10357. .30478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8558. .28868
note="MER58B repeat: matches 23. .337 of consensus"
9639. .29709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="exon boders derived from FGENESH and GENSCAN predictions; true borders could be further down- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="SPTREMBL:Q9HCY7"
translation="FTGASLPAPVISSKNWIRLHFTSDGNHRQRGFSAQYQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MER20 repeat: matches 98. .218 of consensus"
0592. .30802
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note="LTR31 repeat: matches 1. .450 of consensus"
5326. .35657
Sw:033963 Sw:Q05045 Tr:097480 Sw:Q95058 Tr:097131 Sw:P77829 Sw:Q9ZCT7 Sw:085754 Sw:E49464 Tr:Q51919 Sw:P95578 Sw:O80827 Sw:Q94596 Sw:Q60024 Tr:P906622 Sw:O34198 Sw:E51349 Sw:P37282 Sw:P35861 Sw:P35862 Sw:Q05972 Tr:P993570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31220. 31393
//note="MIR repeat: matches 56. .226 of consensus"
32425. .32652
/note="MIR repeat: matches 2. .261 of consensus"
complement(join(32897. .33009,104107. .104314))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not experimental
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/db_xref="G1:12314082"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .247 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 1. .216 of consensus" 1220. .31393
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                                                                                                                                                                     /evidence=not_experimental
complement(24669, .25200)
/note="match: GSS: Em.AQ504827"
complement(25663, .26219)
                                                                                                                                                                                                                                                                                     16085. .26326
/note="match: GSS: Em:AQ463218"
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/hore="match: GSS: Em:AQ347313"
26106. .26574
/hore="match: GSS: Em:AQ405763"
                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ309682"
26085, .26326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="dJ1007G16.2"
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RESULT 9 AC079112/c LOCUS DEFINITION

SOURCE ORGANISM

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED

REFERENCE AUTHORS TITLE JOURNAL REFERENCE

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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: PBACG3.6
NBIGHORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                       The clone sequenced to the left is RPI1-30P5; the clone sequenced to the right is RPI1-474G23. Actual start of this clone is at base position I of RPI1-67K11; actual end is at base position 155888 of RPI1-67K11.
  sequence, see http://genome.wustl.edu/gsc
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/db_xref="taxon:9606"
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/rpt_family="ERV1"
2082. .2215
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2390 . 2801
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+556. .4849
/rpt_family="Alu"
5603. .599^
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2219. .2190
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1746. .3978
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585. .7708
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/rpt_family="Alu"
/709. .7824
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'825. .7905
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1491. .11646
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1181. .4281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="MIR"
1536. .4849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="Alu"
0433. .10741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt family="MIR"
2515. 12833
rpt family="Alu"
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13182. .13483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Alu"
13749. .14156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="L1"
0088. .10108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .13181
                                          SOURCE INFORMATION:
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2910.
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Submitted (07-NOV-2001) Department of Genetics, Washington
Submitted (07-NOV-2001) Department of Genetics, Missouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 16, 2001 this sequence version replaced gi:13752170.

Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
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                                                                                                                                                                                                                          PRI 07-NOV-2001
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4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-MAY-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 155888)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                       Gape
                                                                                                                                                                                                           AC079112 155888 bp DNA linear PRI 07-N
Homo sapiens BAC clone RP11-67K11 from 2, complete sequence.
AC079112
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Goyae,E., Mishra,S. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-67K11
Unpublished
                          Indels
100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (18-AUG-2000) Genome
University School of Medicine,
MO 63108, USA
                                                                                            TGTGGAAGGAATAAATA 82062
                                                                                                                                                                                                                                                                                       AC079112.4 GI:14091934
                                                             1 TGTGGAAGGAATAAATA 17
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Waterston, R.H.
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Waterston, R.H.
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                       Conservative
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Best Local Similarity
Matches 17; Conserv
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AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

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2. (bases 1 to 155165)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bouchagalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, F., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Firzhugh, W., Forrest, C., Galego, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Haeford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Merens, P., McCurk, A., McKernan, K., Norman, C.H., O'Connor, T., O'Donnell, P., Mortow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. Riley, R., Reterson, K., Flexer, N., Eisani, C., Pollars, V., Raymond, C., Riley, R., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., and Zody, M., Yell, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission and Street, Cambridge, MA, 02141, USA, On Apr. 1, 2000 this sequence version replaced gi: 6721267.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                AC021453 156165 bp DNA linear HTG 01-APR-2000
Homo sapiens clone RP11-125C16, WORKING DRAFT SEQUENCE, 14
                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: 155 C 16
Center clone name: 155 C 16
Center clone name: 155 C 16
Center clone name: 155 C 16
Center clone name: 155 C 16
Center clone name: 125 C 16
Center clone name: M3, M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.966731
Consensus quality: 1514142 bases at least Q40
Consensus quality: 151345 bases at least Q20
Consensus quality: 153345 bases at least Q20
Insert size: 160000; agarose-fp
Insert size: 154865; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5169
                                                                                                                                                                                                                                                         1 (bases 1 to 156165)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-125C16
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Web site: http://www-seq.wi.mit.edu
                                                                                                           AC021453
AC021453.3 GI:7382318
                                                                                                                                                                                                                                                                                                                                                (bases 1 to 156165)
                                                                                                                                                                                                                                                                                                                    Unpublished
  RESULT 10
ACO21453
LOCUS
DEFINITION
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rpt_family="MER2_type"
6789. .27175
                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt family="MER1_type"
1829. .22040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .5098, .25143
rpt_family="AT_rich"
5479, .25657
                                                                                                                                                                                                                                                                                                                                                                                       . .20179
family="CT-rich"
. .21686
                                                                                                                                                                                                                                                                              family="AT_rich"
                                                                                                                                                                                                                                       family="GA-rich"
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/rpt family="(CA)n"

30417. 30565

/rpt family="BRVL"

31120. 31275
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/rpt_family="(CA)n"
27536. .27604
/rpt_family="MIR"
27589. .27627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20/89. .27175
/rpt_family="Malk"
/7258. .27307
                                                                                                                                                                                                                                                                                                                                                                     family="(TG)n"
  B. .14654
family="MaLR"
3. .14928
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25658. .25929
/rpt_family="Alu"
25930. .260~~
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/rpt_family="MIR"
28432. .28836
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29950, 30197
/rpt_family="MIR"
30283, 30327
                                                             rpt_family="MaLR"
4990. .15229
                                                                                                      rpt_family="MaLR"
5940. .17923
                                                                                                                /rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="L1"
2757.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .23428
family="Alu"
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8276. .28369
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rpt_family="L2"
6003. .26168
                                                                                                                                                                                           family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565. .24609
pt_family="L1"
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880<u>6</u>.
repeat_region
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1836: contig of 1836 bp in length 1936: gap of 100 bp 5796: contig of 3860 bp in length

1837

126218 TGTGGAAGGAATAATA 126202

1 TGTGGAAGGAATAATA 17

ઠે a PRI 29-AUG-2002

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 157980)
                            AC100852 157980 bp DNA linear PRI 29-AUG-20
Homo sapiens chromosome 17, clone RP11-125C16, complete sequence.
AC100852
                                                                                                                                                                 Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP11-125C16
                                                                           AC100852.2 GI:22539166
HTG.
                                                                                                  Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                          Unpublished
                                      LOCUS
                                                                                                                 ORGANISM
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JOURNAL
               RESULT 11
AC100852
                                                                 ACCESSION
                                                                           VERSION
KEYWORDS
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                                                                                                      SOURCE
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llarity 100.0%; Pred. No. 2.6e+02;
Conservative 0; Mismatches 0; Indels 0;
6: gap of 100 bp

7: contig of 3901 bp in length

7: gap of 100 bp

9: contig of 402 bp in length

9: gap of 100 bp

0: contig of 3381 bp in length

0: gap of 100 bp

0: contig of 3783 bp in length

8: gap of 100 bp

6: contig of 9743 bp in length

6: contig of 10269 bp in length

6: contig of 10269 bp in length

6: contig of 100 bp
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Direct Submission

Submitted (22-NoV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (Dases 1 to 157980)

Barren, B., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaum, C., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cook, A., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Filescand, M., Hage, D., Galagan, J., Gardham, L., Grand-Pierre, M., Hages, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Liu, M., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, M., Macdonald, P., Major, J., Matthews, C., McCarth, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., McZatth, M., Naddrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Naylor, J., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Pierre, N., Rangell, P., O'Neil, D., Olliver, J., Peaners, R., Schauer, S., Schauer, S., Schauer, S., Schauer, R., Schauer, S., Schauer, M., Schauer, B., Stange-Thomann, N., Steaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Steaman, S., Sarnoun, J., Vola, Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Volas, Rahe, S., and Zody, M., Wyman, D., Young, G., Zainoun, J., Raser, S., Shimer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-A0G-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 29, 2002 this sequence version replaced gi:17048222. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washingron.edu/RM/RepeatMasker:html
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Gaps

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repeat_region

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AC024563 158541 bp DNA linear PRI 14-JUL-2002 HOMO sapiens chromosome 19 clone CTC-451A6, complete sequence. AC024563.6 GI:21747460
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AUTHORS
TITLE
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                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla; Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 15841)

2 DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Unpublished

2 (bases 1 to 158541)

5 DOE Joint Genome Institute.

Direct Submission

Losses 1 to 158541)

5 Doe Joint Genome Institute.

Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

8 Jobses 1 to 15844)

Doe Joint Genome Institute and Stanford Human Genome Center.
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1 (bases 1 to 168656)
DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
Direct Submission
                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (01-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell
Submitted Walnut Creek, CA 94598, USA
(bases 1 to 15854)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submission
Submitted (03-0071-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
5 (bases 1 to 158541)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (14-UUL-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 14, 2002 this sequence version replaced gi:15887308.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC009108 168656 bp DNA linear PRI 29-OCT--
Homo sapiens chromosome 16 clone RP11-46309, complete sequence.
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
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Location/Qualifiers
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DOE Joint Genome Institute.
Direct Submission
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AC009108.10 GI:24418066
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Best Local Similarity 100.
Matches 17; Conservative
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             Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 0A AUG 11, 2002 this sequence version replaced gi:20163106. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.

* This sequence of 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp and 100 bp a
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Direct Submission
Submitted (Os-MAR-2000) Multimegabase Sequencing Center, University
Os Washington, PO BOX 357730, Seattle, WA 98195, USA

Madan, M., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,
Nesbitt, R., Traicoff, R., Pleewood, P., Harrison, G., Kaur, A., Madan, A.,
Nesbitt, R., Traicoff, R. and Hood, L.
Direct Submission
Submitted (03-FBB-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NB, Suite 200, Seattle, WA
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Homo sapiens chromosome 15 clone RP11-548M13 map 15q21.3, complete
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1 (bases 1 to 170749)

Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A., Sequencing of human chromosome 15 D15S146-D15S117 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., James, R., Kaur, A., Madan, A., Owen, M.P., Ratcliffe, A., Shaffer, T. and Hood, L.
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On Feb 3, 2001 this sequence version replaced gi:8272670.

Conter: Genome Center
Center: Multimagbase Sequencing Center
Center: Multimagbase Sequencing Center
Center: Attp://chroma.mbt.washington.edu/msg_www
Contect: leerowen@systemsbiology.org
Contect: leerowen@systemsbiology.org
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74310. .141150
/note="assembly_fragment"
141251. .169226
/note="assembly_fragment"
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Chemistry: Dye-terminator Big Dye; 90% of re
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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vector_side:right"
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UWMSC], AC073100 [Drafting center: WUGSC] and AC011912 [Drafting center: UWMSC] were added for finishing
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81160. .81210
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    4093.601 Million cell updates/sec
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		Description	Abk48984 Genomic D	Aak73688 Human imm	Aak73689 Human imm	Aak58790 Human imm	Aat74041 Soybean t	_	Aak73691 Human imm	Aal07315 Human rep		Abz01147 Human leu	Aat20169 Human gen	DNA (S	DNA	DNA	Aah31558 Human olf	Aas90796 DNA encod	Aac59279 Human sec	Aah33029 Human col	Abg81553 Gene up-r	555	e	126332	Abz57733 Human hea
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ABLO5142 ABK48986 ABK48986 ABL361388 ABL70542 ABK742480 ABK742481 ADB60636 AAK70316 ADB60637 AAK70316 AAK80495 AAK80495	ALIGNMENTS	ranso	anti eptide hyper	lifiers t exon	on coding	rnative fi ment of th laim 16"	f Pragment of the in claim 12" 9 g Fragment of the in claim 13" 02 h fragment of the in claim 14"
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Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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              Gaps
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0
              Indels
    Pred. No. 1.3e+02;
; Mismatches 0;
100.0%; Pr
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AAK73688/c
ID AAK73688 standard; DNA; 405 BP
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                                  1 TGTGGAAGGAATAATA 17
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                                                                                                               /*tag= 1
/note= "Fragment of the FOXC2 promoter. Specifically
claimed in claim 1"
claimed in claim 1"
frage . 4629
/*tag= "First exon according to the published form of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes an isolated human FOXC2 promoter region. The mammalian FOXC2 promoter region for the modulation of FOXC2 polypeptide expression has therapeutic value in treating type II diabetes mellitus, obesity, hypercholesterolaemia, other cardiovascular diseases or dyslipidaemias. This sequence encodes the human transcription factor FOXC2, the promoter of which is described in the invention
            /*tag= i
/*tag= i
/note= "Fragment of the POXC2 enhancer. Specifically
claimed in claim 15"
/*tag= k
/*tag= k
/*tag= iFragment of the POXC2 promoter. Specifically
claimed in claim 3"
/*tag= j
/*tag= j
/note= "Fragment of the FOXC2 promoter. Specifically
claimed in claim 2"
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                                                                                                                                                                                                                                                                                                                                              *tag= q
note= "Portion of polypeptide used in alternative
                                                                                                                                                                                                                                                                                                        *tag= r
note= "Second exon according to the alternative
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                                                                                                                                                                                                                                                                           *tag= p
note= "Region coding for DNA-binding domain"
!516, .4629
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                                                                                                                                                                                                                                                       note= "Transcription factor"
448. .2735
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                                                                                                                                                                                                                                             product= "FOXC2"
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10-OCT-2000; 2000US-0238897P.
09-NOV-2000; 2000SE-00004102.
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2516. .3740
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3741. .4629
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     misc_difference 403.
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P-PSDB; AAU79816.
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                                                                                                                                                                                                                                                                                                                                   misc_feature
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2000US-0230438P

06-SEP-2000;

100.0%; Score.17; DB 6; Length 6458;

Query Match

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2000US - 02466119
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) and acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polymucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polymucleotides may be used to produce the secreted (1), by inserting the diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells, AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic represent sequences from the present invention. AAK64942 to AAK54950 and AAM82169 represent invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 28500; 3071pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 405 BP; 126 A; 73 C; 50 G; 156 T; 0 U; 0 Other;
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                                                                2000US-0249299P.
2000US-0249300P.
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2000US-0251479P.
2000US-0251856P.
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                                                                17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
08-DEC-2000;
              17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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24-FEB-2000; 2000US-0180628P.
25-MAR-2000; 2000US-0186464P.
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28-JUN-2000; 2000US-011486FP.
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11-JUL-2000; 2000US-01144FP.
11-JUL-2000; 2000US-
                            WO200157182-A2
Homo sapiens
                                                                                      17-JAN-2001;
                                                         09-AUG-2001
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14-AUG-2000;
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14-AUG-2000;
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01-SEP-2000;
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12-SEP-2000
14-SEP-2000
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polyunclectides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
polynucleotides may be used to produce the secreted (1), by inserting the
nucleic acids into a host cell and culturing the cell to express the
chack and treat immune/haematopoietic related diseases, especially
cancers and cancer metastases of haematopoietic artigen genomic
cancer metastases of haematopoietic artigen genomic
sequences from the present invention. AAK45492 to AAK5450 and AAM82169
represent sequences used in the exemplification of the present invention
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                                                                                                          Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3850.
                                                                                                                                                                               Disclosure; SEQ ID NO 28501; 3071pp + Sequence Listing; English.
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AAK58790/C

ID AAK58790 standard; cDNA; 418 BP
XX

AC AAK58790;
XX

DT 06-NOV-2001 (first entry)
XX

Human; immune; haematopoietic ant:
XX

Human; immune; haematopoietic;
XX

COS Homo sapiens.
XX

NO200157182-A2.
XX

PN WO200157182-A2.
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PN WO20015718-A2.
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                      Ruben SM
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Best Local Similarity 100..
                   Rosen CA, Barash SC,
                                                                WPI; 2001-483426/52.
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20-OCT-2000; 2000US-0241826P.
01-NOV-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246477P.
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08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Barash SC, Rosen CA,

WPI; 2001-483426/52 P-PSDB; AAM86009 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis. useful for preventing,

Claim 1; SEQ ID NO 3850; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM9121. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the

Length 1807;

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Score 16;

94.1%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a novel thiol protease D3-alpha derived from germinated soybean cotyledon. A method for the production of thiol protease using Escherichia coli transformed with recombinant expression vectors containing a DNA sequence encoding thiol protease has been produced. The method can be used to prepare large amounts of thiol protease with high efficiency
nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK8764 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK64942 to AAK64950 and AAW82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         cotyledon; germinate; transformant; Escherichia coli; ant expression vector; ds.
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                                                                                                                                                 Length 418;
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100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0;
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68. .460

/*rag= b

461. .1459

/*rag= c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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95JP-00245279.
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Best Local Similarity 100.0
Matches 16; Conservative
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30-AUG-1995;
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                                        Gaps
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                                     Indels
      Pred. No. 3.8e+02; Mismatches 0;
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AAK73690/C

ID AAK73690;

XX

AAK73690;

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C 07-NOV-2001 (first entry)

XX

DT 07-NOV-2001 (first entry)

XX

Human immune/haematopoietic antige

XX

Human; immune; haematopoietic; imm

XW

Cytcstatic; gene therapy; vaccine;

XX

Homo sapiens.

XX

WO200157182-A2.

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O9-AUG-2001.

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17-JAN-2001; 2001WO-US001354.

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17-JAN-2001; 2001WO-US001354.

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YA-FEB-2000; 2000US-018662EP.

PR 31-JAN-2000; 2000US-018664P.

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PR 19-MAY-2000; 2000US-019813P.

PR 19-MAY-2000; 2000US-018664P.

PR 19-MAY-2000; 2000US-018664P.

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PR 19-MAY-2000; 2000US-019813P.

PR 19-MAY-2000; 2000US-019813P.

PR 11-UUL-2000; 2000US-021646P.

PR 11-UUL-2000; 2000US-021646P.

PR 11-UUL-2000; 2000US-021646P.

PR 11-UUL-2000; 2000US-02164P.

PR 11-UUL-2000; 2000US-022566P.

PR 14-AUG-2000; 2000US-022575P.

PR 14-AUG-2000; 20
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2000US-0232398P.
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2000US-0205515P.
2000US-0205515P.
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2000US-0230437P.
2000US-0230438P.
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2000US-0180628P.
2000US-0184664P.
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08-SEP-2000;
08-SEP-2000;
    Homo sapiens.
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                                                       09-AUG-2001
  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) and can be used in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polyunclectides may be used in the prevention, diagnosis and transparent of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting the price acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectics may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers from the present invention. AAK64902 to AAK87890 and AAM82169 sequences from the present invention. AAK64902 to AAK84900 and AAM82169 represent invention
                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 28502; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9124 BP; 3077 A; 1494 C; 1554 G; 2999 T; 0 U; 0 Other;
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100.0%; Pred. No. 4.2e+02;
ive 0; Mismatches 0; Indels
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AAK73691/c
ID AAK73691 standard; DNA; 21619 BP.
XX
AC AAK73691;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen
XX
KW Human; immune, haematopoietic; immu
KW CYtostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                          Rosen CA, Barash SC, Ruben SM,
17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-025991P.
01-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025103P.
05-DEC-2000; 2000US-025103P.
06-DEC-2000; 2000US-025105P.
08-DEC-2000; 2000US-025105P.
08-DEC-2000; 2000US-025105P.
08-DEC-2000; 2000US-0251069P.
08-DEC-2000; 2000US-0251069P.
08-DEC-2000; 2000US-0251069P.
08-DEC-2000; 2000US-0251069P.
08-DEC-2000; 2000US-0251069P.
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Best Local Similarity 100.
Matches 16, Conservative
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2000US-0250391P.
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
coctivity, and can be used in gene therapy and vaccine production. (I)
corporation and polynuclectides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
consplement the patients own production of (I). Additionally, (S)
copynuclectides may be used to produce the secreted (I), by inserting the
concleic acids into a host cell and culturing the cell to express the
concleic acids into a host cell and culturing the cell to express the
concern and treat immune/haematopoictic-related diseases, especially
cancers and cancer metaetases of haematopoictic derived cells. AAK64703
concern and cancer thuman immune/haematopoictic antigen genomic
concerns and present human immune/haematopoictic antigen genomic
concerns and cancer metaetases of haematopoictic antigen genomic
concerns and cancer invention. AAK54942 to AAK54950 and AAM62169
concerns error metaetases of haematopoictic cerived cells.
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                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
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                                                                                                                                          Disclosure; SEQ ID NO 28503; 3071pp + Sequence Listing; English.
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Pred. No. 4.4e+02;
0; Mismatches 0; Indels
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100.0%; Pre
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AAL07315/c
ID AAL07315 standard, DNA, 21619 BP.
                 Ruben SM
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04-FEB-2000; 2000US-0186628P.
24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0189374P.
11-MAR-2000; 2000US-0190076P.
118-APR-2000; 2000US-0191379.
19-MAY-2000; 2000US-0205515P.
07-UUN-2000; 2000US-0205515P.
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2000US-0215135P.
2000US-0216647P.
2000US-0216880P.
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Best Local Similarity 100.
Matches 16; Conservative
               Rosen CA, Barash SC,
                                                   WPI; 2001-483426/52.
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07-JUL-2000
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PR 11-TUL_2000; 2000US-0217487P.

PR 11-TUL_2000; 2000US-0217487P.

PR 14-MIC-2000; 2000US-0218289E.

PR 14-MIC-2000; 2000US-022813P.

PR 22-MIC-2000; 2000US-022813P.

PR 22-MIC-2000; 2000US-022813P.

PR 22-MIC-2000; 2000US-022813P.

PR 22-MIC-2000; 2000US-022813P.

PR 23-MIC-2000; 2000US-023813P.

PR 23-MIC-2000; 2000US-023813P
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
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2000US-0241826P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-465570/50.
20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - OCT - 2000; 20 - O
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Gaps

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94.1%; Score 16; DB 4; Length 21619; ilarity 100.0%; Pred. No. 4.4e+02; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 16; Conserv

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06-SEP-2000; 2000US-0230438P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231413P.
14-SEP-2000; 2000US-023149P.
13-OCT-2000; 2000US-0231444P.
13-OCT-2000; 2000US-024444P.
13-OCT-2000; 2000US-0234444P.
13-OCT-2000; 2000US-0234444P.
13-OCT-2000; 2000US-0234444P.
13-OCT-2000; 2000US-0234444P.
13-OCT-2000; 2000US-0234444P.
13-OCT-2000; 2000US-0234444P.
13-O
   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
                                                                                                                                                                Human ovarian and breast cancer associated polymucleotide SEQ ID NO 977
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The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; ostecarthritis; cytomegalovirus; infection; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
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Ly N, Woodward R, Quertermous T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene signature HUMGS01315.
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Best Local Similarity 94.1%;
Matches 16; Conservative
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                                                                                                                                          WO200257414-A2.
                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (ABA07454-ABA08224) and proteins (ABB10743-ABB10880) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune breast, gastroinment thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumacid arthritis and ulcerative colifis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. creebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parsaitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T7; leukocyte; gene expression profiling; allograft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 977; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.1%; Score 16; DB 4; Length 21619; 100.0%; Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                         17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-02590P.
01-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025193P.
05-DEC-2000; 2000US-025199P.
05-DEC-2000; 2000US-02519P.
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                                                                                                                                                                                                                                                                                                                                                                        08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-025499P.
05-JAN-2001; 2001US-025678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488786/53.
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                                                                     17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
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Skokut T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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                                                                                                                                                                             A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, DNA or mRNA is claimed The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'- untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular is sue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types
                                                                                                            Single-stranded DNA for identifying gene signatures - isolated from 3'-directed human cDNA library that reflects relative abundance of corresp. mRNA in specific human tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; visual phenotype; plant; architecture; leaf surface; chlorotic; bleaching; etching; wet leaf; stunting; elongation; texture; agronomic trait; growth regulation; dwarf variety; insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                     Sequence 215 BP; 71 A; 32 C; 36 G; 72 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Larrinua I,
                                                                                                                                                          Claim 1; Page 577; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruegger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD17249 standard; DNA; 601 BP
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DOW AGROSCIENCES LLC.
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            93JP-00355504
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                                                                 Matsubara K, Okubo K;
                                (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-300858/29.
                                                                                         WPI; 1995-206931/27
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nes 16; Conserv
                                            OKUBO K.
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            L2-NOV-1993;
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                                              (OKUB/)
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This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Purthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual plantucleotides described herein. This polynucleotide is a homologue of a DNA sequence that confers an altered visual phenotype when expressed in
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Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for conferring altered visual phenotypes in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (SeqID 1914) that confers an altered visual phenotype in plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 601 BP; 178 A; 105 C; 148 G; 170 T; 0 U; 0 Other;
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                                                                                                                                                                          Claim 1; SEQ ID NO 1317; 517pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plants, the method of the invention.
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(DOWC ) DOW AGROSCIENCES LLC.
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This invention relates to the identification and isolation of movel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wer leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these movel phenotypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed sensescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises generating transgenic plants as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the phenotype of plants each, plant tissues and plant cells containing the DNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.
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Sequence 601 BP; 178 A; 105 C; 148 G; 170 T; 0 U; 0 Other;

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Gaps
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     90.6%; Score 15.4; DB 9; Length 601; 94.1%; Pred. No. 6.9e+02; ive 0; Mismatches 1; Indels (
Query Match
Best Local Similarity 94.15
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8 9 RESULT 14

ADD16351 standard; DNA; 602 ADD16351; ADD16351

BP.

ds; visual phenotype; plant; architecture; leaf surface; chlorotic; bleaching; etching; etching; teching; taying trait; growth regulation; dwarf variety; insect resistance; heat stress; transgenic. DNA (SeqID 419) that confers an altered visual phenotype in plants. (first entry) 15-JAN-2004

WO2003020741-A1

13-MAR-2003

30-AUG-2002; 2002WO-US027880

31-AUG-2001; 2001US-0316326P

(DOWC) DOW CHEM CO. (DOWC) DOW AGROSCIENCES LLC.

Shukla V; Ruegger M, Larrinua I, Crosley R, Skokut T, WPI; 2003-300858/29 Oryzae

Novel isolated nucleic acid derived from Nicotiana benthamiana, C sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for conferring altered visual phenotypes in plants. Claim 1; SEQ ID NO 419; 517pp; English This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf

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varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the polymucleotides described herein. This polymucleotide is a homologue of a DNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.
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Sequence 602 BP; 182 A; 106 C; 145 G; 169 T; 0 U; 0 Other;

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90.6%; Score 15.4; DB 9; Length 602; 94.1%; Pred. No. 6.9e+02; ive 0; Mismatches 1; Indels 0
                   Local Similarity 94.1 ses 16; Conservative
     Query Match
                                       Matches
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8 셤 RESULT 15 AAH31558

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ВР. AAH31558 standard; cDNA; 657

AAH31558;

(first entry) 30-JUL-2001

Human olfactory receptor polynucleotide, SEQ ID NO: 131

Human, olfactory receptor, OR, primary scent determination, secondary scent determination, polypeptide library, odour receptor; scent profile; scent fingerprint; scent representation; ss.

Homo sapiens.

WO200127158-A2

19-APR-2001

06-OCT-2000; 2000WO-US027582.

99US-0158615P. 24-FEB-2000; 2000US-0184809P 08-OCT-1999;

(DIGI-) DIGISCENTS. (YEDA) YEDA RES & DEV CO LTD.

Yanai I; Fuchs T, Lancet D, Glusman G, Bellenson J, Smith D,

WPI; 2001-290713/30.

New polynuclectides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists.

Claim 1; Fig 2; 1857pp; English.

encode polypeptides involved in olfactory sensation. The polymudleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the adour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a series entering such secondary scents. This enables the construction of a sepsessentation (also called a scent fingerprint or scent profile), which receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining the differences in the olfactory faculties of different individuals The present sequence is one of a number of isolated polynucleotides which

Sequence 657 BP; 171 A; 124 C; 160 G; 165 T; 0 U; 37 Other;

Query Match 90.6%; Score 15.4; DB 4; Length 657; Best Local Similarity 94.1%; Pred. No. 6.9e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps

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Search completed: March 25, 2004, 10:25:16 Job time: 21.642 secs

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1 (bases 1 to 362)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, X., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z., Gu, W., Huang, W., Zhao, X., Insight into hepatocallular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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AQ247792 HS_2063_A
                                                                                         March 25, 2004, 09:53:09; Search time 128.47 Seconds (without alignments) 3951.570 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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El (bases 1 to 411)

Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S.

ESTS of Japanese morning glory

Unpublished (2002)

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National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Fax: 81-559-81-6855
                                                                                                                        1.362

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BJ577286 GI:27259114
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/cultivar="Tokyo-kokei standard"
/db_xref="taxyo:15883"
/clone="jm34k01"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower
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Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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RESULT 3 AQ080438

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Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a rendom human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)
Other GSse: CIT-HSP-2382B13.TR
Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are avallable from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
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AQ080438 445 bp DNA linear GSS 20-AUG-1998 CIT-HSP-2382B13.TF CIT-HSP Homo sapiens genomic clone 2382B13, genomic survey sequence.
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1. 445
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AQ247792
AQ247792.1 GI:3697974
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AQ080438.1 GI:3441622
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Homo sapiens
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Homo sapiens
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Query Match
Best Local Similarity
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BJ572614/c
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BJ571448/c
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (bases 1 to 652)
3 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
AL Unpublished (1998)
Other_GSSs: CIT-HSP-2342D16.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: madamsektigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ055707 652 bp DNA linear GSS 30-JUL-1998
CIT-HSP-2342D16.TR CIT-HSP Homo Rapiens genomic clone 2342D16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                /sex="male"
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels
             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington Worth, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Teal: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2063 row: M column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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clone="342D16"
/sex="Male"
/cell_type="Sperm"
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Location/Qualifiers
1. 510
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AQ055707
AQ055707.1 GI:3352313
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Homo sapiens
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BJ572614 Ipomoea nil mixture of flower and flower bud Ipomoea nil cDNA clone jm21e10 3', mRNA sequence.
BJ572614.1 GI:27254442
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BJ571448 I GI:27253276
EST.
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(Dases 1 to 684)
Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. Unpublished (2002)
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/db_xref="intho-kokei standard"
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Ipomoea nil
Bikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamides; Solanales; Convolvulaceae; Ipomoea.
1 (bases 1 to 773)
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/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Wishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                  ch 100.0%; Score 17; DB 28; 1 Similarity 100.0%; Pred. No. 2.2e+03; 17; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyea; eudicoryledons; core eudicots; asterior asterior and ida; Solanales; Convolvulaceae; Ipomocea.

1 (Dases 1 to 791)
1 (Dases 1 to 791)
2 Hoshino, A., Seki, M., Shin i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. ESTS of Japanese morning glory
2 Unpublished (2002)
2 Contact: Tadasu Shin-i
3 Contact: Tadasu Shin-i
4 Center For Genetic Resource Information
5 National Institute of Genetics
6 Ill Yata, Mishina, Shizuoka 411-8540, Japan
7 Tel: 81-559-81-6855
7 Fax: 81-559-81-6855
                                                                                  BJ567603 Ipomoea nil mixture of flower and flower bud Ipomoea nil BJ567603 Ipomoea nil mixture of elower and flower bud Ipomoea nil BJ567603 Igi:27249423 EST.
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BJ570146 G1:27251974
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[ Dases 1 to 814)
Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitaaaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. ESTs of Japanese morning glory
Contact: Tadasu Shin-i
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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Location/Qualifiers
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          72 TGTGGAAGGAATAAATA 56
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BJS67603/c
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Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitaska, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. ESTS of Japanese morning glory
Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: For Genetic Resource Information
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Fax: 81-559-81-6656
Fax: 1-559-81-6656
Fax: 1-6056
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1 (Dases 1 to 781)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Nitaeaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S. Unpublished (2002)
Contact: Tadasu Shin-i
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
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100.0%; Score 17; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 /organism="Ipomoea nil"
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/db xref="taxon:35883"
/clone="jm17k24"
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/cultivar="Tokyo-kokei standard"
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Location/Qualifiers
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Gaps

Email: tshini@genes.nig.ac.jp

FEATURES

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Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledone; core eudicots; asterida; lamiida; Solanales; Convolvulaceae; Ipomoea.

E 1 (bases 1 to 831)
S Hoshino,A., Seki,M., Shin i,T., Carninci,P., Kamiya,A., Shiraki,T., Nitasasa,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
ESTS of Japanese morning glory
L Unpublished (2002)
Contact: Tadasu Shin-i,
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1179 bp mRNA linear EST 23-WAY-2005
AL526913 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CSODC017XM10 5-PRIME, mRNA sequence.
AL526913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Ipomoea nil"
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/note="Tiss strand cDNA was primed with a NotI-oligo(dT)
/note="Tis prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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1 (Dases 1 to 1179)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Unpublished (2001)

On Peb 13, 2001 this sequence version replaced gi:12790406.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: sequefégenoscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODCO17BG05QP1.
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  Ipomoea nil (Japanese morning glory)
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Bmail: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Homo sapiens
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nes 17; Conservative
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1 (Dases 1 to 815)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S. Unpublished (2002)
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/mol_type="mRNA"
/cultivar="Toxyo-kokei standard"
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/db_xref="inacon:35883"
/clone="inacon3"
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/clone_lib="Ipomoea nil mixture of flower and flower bud"
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BJ578691.1 GI:27260519
EST.
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BJ569616 Ipomoea nil mixture of flower and flower bud Ipomoea nil
CDNA clone jm6c03 3', mRNA sequence.
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100.0%; Score 17; DB 12; Length 815;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels C
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fat: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [pomoea nil (Japanese morning glory)
                                                     organism="Ipomoea nil"
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Matches 17; Conservative 0;
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URL.http://genome.gsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Casaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M.,
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E 1 (bases 1 to 217)

S Konno, H. Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Fukuda, S., Pukunishi, Y., Harakawa, T., Fukuda, S., Pukunishi, Y., Harakawa, T., Hozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kikuchi, N., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, N., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shibata, Y., Shigama, A., Shinagawa, A., Shinaga, Y., Suzuki, H., Taqawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yomida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                            BB330439 LIKEN full-length enriched, 6 days neonate medulla oblongata Mus musculus cDNA clone B730013P22 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-2 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                        Length 1179;
                                                                                 95.3%; Score 16.2; DB 9; Length 1 llarity 88.2%; Pred. No. 4.6e+03; Conservative 2; Mismatches 0; Indels
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Unpublished (2000)
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                                                                                                                 Similarity
                                                                                 Query Match
Best Local Simil
Matches 15, C
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SOURCE
ORGANISM
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci, P., Nishiyama, Y., Westover, A., Itch, M., Nagacka, S.,
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Trennostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itch, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB331990 BKEN full-length enriched, 6 days neonate medulla oblongata Mus musculus cDNA clone B730041N08 3', mRNA sequence.
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
/clone lib="RIKEN full-length enriched, 6 days neonate medulla oblongata"
//note="Site_1: Sale1" | Site_2: BamHI, cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was changed with a primer [8]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mus musculus
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Best Local Similarity
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Query Match
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0;

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Gaps

1 TGTGGAAGGAATAAT 16

106 TGTGGAAGGAATAAAT 121

Search completed: March 25, 2004, 15:30:09 Job time : 133.47 secs Sequence 1028, Apprendence 2, Appli Sequence 29, Appli Sequence 29, Appli Sequence 10, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1770, Appli Sequence 260, Appli Sequence 260, Appli Sequence 260, Appli Sequence 1097, Appli Sequence 1097, Appli Sequence 1097, Appli Sequence 1097, Appli Sequence 1097, Appli Sequence 1185, Appli Sequence 1185, Appli Sequence 1185, Appli Sequence 1185, Appli Sequence 1186, Appli Sequence 1186, Appli Sequence 1186, Appli

Seguence Seguence 1

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APPLICANT: C. Frank Behnert
APPLICANT: C. Frank Behnert
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANIIEBNSE MODULATION OF INTERFERON GAMMA RECEPTOR 1 EXPRESSION
FILE REFERENCE: RTG-0234
CURRENT APPLICATION NUMBER: US/09/843,376
CURRENT FILING DATE: 2001-04-26
NUMBER OF SEQ ID NOS: 88
SEQ ID NO 10
LENGTH: 26000
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APPLICANT: Buechler, Joe
APPLICANT: Walkirs, Gunars
APPLICANT: Gray, JGF
APPLICANT: Corberg, Nis
FILE REFERENCE: 020015-000200US
CURRENT APPLICANT: NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 999
                           US-08-887-5348-29
US-09-527-431-29
US-09-743-871B-10
US-09-743-871B-10
US-08-751-871-1
US-08-72-055-2
US-08-72-055-2
US-08-72-077-1
US-09-620-312D-260
US-10-204-708-70
US-09-620-312D-135
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US-09-620-312D-135
US-09-620-312D-135
US-09-620-312D-135
US-09-620-312D-135
JS-09-107-532A-1028
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US-08-956-171E-85
US-08-961-527-139
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94.1%; Pred. No. 95;
iive 0; Mismatches
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Sequence 997 Application US/09456090A
; Patent No. 6680209
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Best Local Similarity 94.1
Matches 16; Conservative
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22190
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33742
51173
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8351
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ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (1)..(675)
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US-09-843-376-10
                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 65
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Sequence 1, Appli
Sequence 1175, A
Sequence 1, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 16, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
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Sequence 53, Appli
Sequence 2, Appli
Sequence 26, Appli
Sequence 7, Appli
Sequence 335, App
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Sequence 99, Appl
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4, Appli
                                                                                                               March 25, 2004, 09:55:14; Search time 3.34382 Seconds (without alignments) 2821.370 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-620-651-11
US-09-500-651-1
US-09-390-412B-1
US-09-390-412B-1
US-09-744-675-3
US-09-128-155-16
US-09-128-155-17
US-09-428-155-17
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US-09-568-816A-7
US-09-328-111-335
US-09-091-590A-4
US-09-328-111-533
US-08-998-416-353
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US-09-301-665-3
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                                                                                                                                                                                                                                                                                                                   682709 seqs, 277475446 residues
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17
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length
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16592
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Perfect score:
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                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDLUN TYPE: FLORM:

MEDLUN TYPE: FLORM:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/169,119

FILING DATE: 09-Oct-1998

CLASSIFICATION: -Unhown>

ATTORNEY/AGENT INFORMATION:

NAME: Kettelberger, Denise M.

TELECOMONICATION INFORMATION:

TELECOMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: 1...313
OTHER INFORMATION: /standard_name= "Rabbit CDNA
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Patent No. 6639063

GENERAL INPORMATION:
APPLICANT: Jobert, S.
APPLICANT: Glockano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2

CURRENT FAPLICANTON NORSER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 11175

LENGTH: 391
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence S1-1"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 713-850-0909
TELEX: 713-850-0165
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 TGTGGAAGGAAGAAT 175
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  NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.8
Matches 15, Conservative
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Matches 15; Conservative
                                                                                 CITY: Houston
STATE: Texas
COUNTRY: USA
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Patent No. 6264953
GENERAL INFORMATION:
GENERAL INFORMATION:
Method of Preparation and Use for Zona
TITLE OF INVENTION: Method Antigens and Antibodies for Sterilization and
Contracept
                                                                                                                                                                                                                                                                                                                                                                                         Method of Preparation and Use for Zona
Pellucida Antigens and Antibodies for Sterilization and
Contraception
                                                                                                            ;
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                                                            DB 4; Length 675; 96;
                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: TEXAS
COUNTRY: USA
ZIP: 77027
COMPUTER TEADABLE FORM:
COMPUTER TEADABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,452
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Pravel, Hewitt, Kimball & Krieger
1177 West Loop South, 10th Floor
                                                              Score 15; DB 4; Pred. No. 96; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TLING DATE: 30-ARR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger. Denise M.
TELEPHONE: 713-850-0999
TELEPHONE: 713-850-0909
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 base pairs
                                                                                                                                                                                                                                                                          US-08-396-452-1/C

Sequence 1, Application US/08396452
Fatent No. 5820863

GENERAL INFORMATION:
APPLICANT: Dunbar, Bonita S.
TITLE OF INVENTION: Method of Prep TITLE OF INVENTION: Pellucida Anti TITLE OF INVENTION: Contraception; NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimba
                                                              Query Match
Best Local Similarity 100.0%; P:
Matches 15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 TGTGGAAGAATAAAT 83
                                                                                                                                                                                           162 İĞGAAĞGAATAATA 176
                                                                                                                                                    3 TGGAAGGAATAATA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 313 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
; OTHER INFORMATION: M2-20H
US-09-456-090A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: CDNA
US-08-396-452-1
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US-09-169-119-1/c
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Sequence 1, Application US/08813591

Sequence 1, Application US/08813591

Patent No. 5824534

GENERAL INFORMATION:
APPLICANT: RAMAI MISAKO
APPLICANT: RAMAI MISAKO
APPLICANT: NUMA, TETSITA
APPLICANT: NUMA, TETSITA
APPLICANT: NUMANIONE MINA, TETSITA
APPLICANT: NOERTION:
TITLE OF INVENTION: AMINOPEPTIDASE GX, AND A METHOD OF
TITLE OF INVENTION: AMINOPEPTIDASE GX, AND A METHOD OF
TITLE OF INVENTION: AMINOPEPTIDASE GX, AND A METHOD OF
STRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
APPLESSEE: P.C.
STREET: 1755 S. JEFPERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OFFRAILING SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/813.591
FILING DATE: 08-MAR-1997
FILING DATE: 08-MAR-1997
APPLICATION NUMBER: JP 051848/1996
PRILING DATE: 08-MAR-1997
APPLICATION NUMBER: JP 030458/1997
APPLICATION NUMBER: JF 030458/1997
APPLICATION NUMBER: JC 4618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 10-845-0
TELEPHONE: 703-413-3000
TELEFRA: 703-413-3200
TELEFRA: 703-413-3200
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                          Sequence 1, Application US/09500651
GENERAL INFORMATION:
APPLICANT: ASANO, MINAO
APPLICANT: KAMAI, MISAKO
APPLICANT: MITAA, TETSUVA
APPLICANT: NIO, NORIKI
ITLE OF INVENTION: AMINOPEPTIDASE GX, AND A METHOD OF
ITLE OF INVENTION: HYDROLYSING A PROTEIN WITH THE SAME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CORREST: ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: ADDRESSEE: P.C.
ADDRESSEE: P.C.
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84.7%; Score 14.4; DB 1; Length 1056;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0
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OTHER INFORMATION: /note= "INSERTION SEQUENCE, METHOD
OTHER INFORMATION: OF DETERMINING THE CHARACTERISTICS: E"
US-09-500-651-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "METHOD OF DETERMINING THE CHARACTERISTICS: P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
FRICK APPLICATION DATA:
PRICK APPLICATION UNDRER:
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-845-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/813,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 703-413-3000
TELEPACY: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1056 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: cDNA to m
ORIGINAL SOURCE:
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 1..1056
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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Gaps
                                                                                                                                                                                                                                                                                                                                                            Query Match

84.7%; Score 14.4; DB 1; Length 1056;

Best Local Similarity 93.8%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                            /note= "INSERTION SEQUENCE, METHOD OF DETERMINING THE CHARACTERISTICS: E"
                                                                                                                                                          /note= "METHOD OF DETERMINING THE CHARACTERISTICS: P"
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1056
OTHER INFORMATION: CHARACTEI
OTHER INFORMATION: CHARACTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 GTAGAAGGAATAAATA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GTGGAAGGAATAATA 17
                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                         LOCATION: 1..9
OTHER INFORMATION:
OTHER INFORMATION:
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RESULT

Gaps

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436 GTAGAAGGAATAATA 451

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RESULT 12
US-09-495-050A-121
US-09-495-050A-121
Sequence 121, Application US/09495050A
Parent No. 6492505
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Gueddy
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED E
FILE REPERENCE: PA-013 US
CURRENT APPLICATION NUMBER: US/09/495,050A
CURRENT FILING DATE: 2000-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL WIS THEREOF
; FILE REPERENCE: 19944/05201
; CURRENT APPLICATION NUMBER: US 60/091,650
; EARLIER PLILING DATE: 1998-07-02
; EARLIER PLILING DATE: 1998-07-02
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NOS: 18
; SEQ ID NOS: 18
; SEQ ID NOS: 18
; SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.7%; Score 14.4; DB 3; Length 176373; 93.8%; Pred. No. 3.6e+02; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

84.7%; Score 14.4; DB 3; Length 152331;
Best Local Similarity 93.8%; Pred, No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0;
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 16
LENGTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
TYPE: DNA
ORGANISM: HOMO Sapiens
                                                                                                                                                                                                                                                   FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(152331)

OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature;
| NAME/KEY: misc_feature;
| LOCATION: (1)...(176373)
| OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105263 TGTGGAAGCAATAAAT 105248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78207 TGTGGAAGCAATAAAT 78222
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 176373
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US-09-128-155-17
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                                                                          GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
ITILE OF INVENTION: Nucleic acids encoding mammalian interleukin-lzeta, related reage
TITLE OF INVENTION: methods
FILE REFERENCE: DX0904K
CURRENT APPLICATION NUMBER: US/09/398,4128
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: US 60/100948
PRIOR FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOORG62
CURRENT APPLICATION NUMBER: US/09/734,675
CURRENT APPLICATION NUMBER: US/09/734,675
SUPPREMENT: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 300.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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APPLICANT: Pan, Yang
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: US 0404/052001
CURRENT APPLICATION UNDER: US/09/128,155
CURRENT FILLNG DATE: 1998-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.7%; Score 14.4; DB 4; Length 1225; 93.8%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Patent No. 6117654
                          ; Sequence 1, Application US/09398412B
; Patent No. 6680380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09734675
Patent No. 6365391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30049 TGTGGAAGGGATAAAT 30064
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1225
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Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: CDS
; LOCATION: (491)..(1144)
; OTHER INFORMATION:
US-09-398-4128-1
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Human
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US-09-128-155-16/c
        US-09-398-412B-1/c
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US-09-734-675-3
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| Sequence 4, Application US/08392546C
| Patent No. 5874298
| GENERAL INFORMATION:
| APPLICANT: Johnson, Janice, Kral, Robert M. Jr., Krapcho, Kare:
| TITLE OF INVENTION: Insecticidal Toxins from Bracon hebetor NUMBER OF SEQUENCES: 11
| CORRESPONDENCE ADDRESS: ADDRESSE: MADSON & METCALF |
| STREET: 950 FIRST INTERSTATE BUILDING |
| STREET: 170 SOUTH MAIN STREET |
| STATE: UTAH |
| STATE: UTAH |
| STATE: UTAH |
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ZIP: 84101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM MS-DOS
OFFWATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,546C
FILING DATE: 2/17/95
ATTORNEY/AGENT INFORMATION:
NAME: L. CRAIG METCALF
REGISTRATION NUMBER: 1094.2.3
TELECOMCUNICATION INFORMATION:
TELECOMCUNICATION INFORMATION:
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TELECOMCUNICATION INFORMATION:
TELECOMCUNICATION INFORMATION R APPLICATION NUMBER: 60/118,318

PRIOR FILING DATE: February 1, 1999

NUMBER OF SEQ ID NOS: 305

SOCTWARE: PERL Program

SEQ ID NO 121

LENGTH: 234

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID NO. 6492505 1386485CT1

US-09-495-050A-121
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82.4%; Score 14; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0;
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; INDIVIDUAL ISOLATE: 30 kDa toxin cDNA
US-08-392-546C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 TGGAAGGAATAAAT 184
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HYPOTHETICAL:
ANTI-SENSE: Yes
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ORIGINAL SOURCE:
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| Gequence 53, Application US/08956171B
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| Gequence 53, Application US/08956171B
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; FILE REFERENCE: UTSH:243
; CURRENT APPLICATION NUMBER: US/09/301,665
; CURRENT APPLICATION NUMBER: 06/083,408
; EARLIER APPLICATION WUMBER: 60/083,408
; EARLIER FILING DATE: 1998-04-28
; EARLIER FILING DATE: 1998-04-28
; SAFURME: PATON NUMBER: 60/083,370
; EARLIER FILING DATE: 1998-04-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PATON NOS: 4
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; SOFTWARE: PATON NOS: 4
; SOFTWARE: PATON NOS: 4
; SOFTWARE: PATON NOS: 4
; SOFTWARE: PATON NOS: 4
; SOFTWARE: PATON NOS: 4.98+02;
MATCHES 14; CONSERVATIVE 0; Mismatches 0; Indels 0; Gaps
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Search completed: March 25, 2004, 15:34:21 Job time: 4.34382 secs

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March 25, 2004, 07:40:23 ; Search time 25:9441 Seconds (without alignments) 4093.601 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                        3373863 seqs, 2124099041 residues
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                                                                    OM nucleic - nucleic search, using sw model
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length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abk48986 Genomic D	Abk48984 Genomic D	Ada72007 Rice gene	Continuation (2 of	Ach39191 Human foe		Aaf54867 Nucleotid	Aaf54868 Genomic n	Abx96482 Rice endo		Abl22340 Drosophil		Continuation (11 o	Abs77078 Frog embr	Aak75882 Human imm	Aas35994 Human car	Ade46688 Human car	Aak75883 Human imm	Adc86642 Human GPC	Adc86940 Human GPC		Aas67702 DNA encod	OKOT KONCYCIK
SUMMARIES	ID	ABK48986	ABK48984	ADA72007	ABQ84281 1	ACH39191	ACH40492	AAF54867	AAF54868	ABX96482	ACA34306	ABL22340	AAT42063 09	AAT42063_10	ABS77078	AAK75882	AAS35994	ADE46688	AAK75883	ADC86642	ADC86940	ADC87619	AAS67702	DDC42004
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	Score	25	25	19.8	19.2	18.8	18.8	18.8	18.8	18.6	18.4	18.4	18.4	18.4	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	17.8	17.8
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AAC36140	AAS46615	ABQ67083	AAZ01425_07	ABX81735	ADE72935	ADE72934	ACA44731	AAC55313	ABL32534	AAC55339	ABS73286	ABL33082	ABL34528	ABL70253	ADB54263	ABS55500	ACA62841	AAX33645	AAX88653	ABZ14962	AB070281	
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17.8	17.8	17.8	17.8	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.4	17.4	17.4	17.4	
c 24		c 26	27	28	c 29	m	31	32	33	34	35	36	m	38	n	4,	41	c 42	2 43	4	C 45	

ALIGNMENTS

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Transcription factor; FOXC2; antidiabetic; anorectic; antilipaemic; cardiovascular; FOXC2 promoter; cardiovascular; FOXC2 promoter; diabetes mellitus; obesity; hypercholesterolaemia; dyslipidaemia; cardiovascular disease; mouse medenchyme forkhead 1; MHF-1; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated FOXC2 promoter region that modulates the expression of a FOXC2 polypeptide is useful for treating obesity and type II diabetes mellitus.
                                                                                  Genomic DNA encoding mouse mesenchyme forkhead-1 (MHF-1)/FOXC2
                                                                                                                                                                                                                            <u>-</u>
                                                                                                                                                                                Wasserman WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 22; Page 45-46; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                  Rondahl L,
                    BP.
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10-OCT-2000; 2000US-0238897P.
09-NOV-2000; 2000SE-00004102.
                      ABK48986 standard; DNA; 6021
                                                                                                                                                                                                                                                                                             26-SEP-2001; 2001WO-SE002098
                                                               (first entry)
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P-PSDB; AAU79818.
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                                                                                                                                                                Mus musculus
                                                                 02-JUL-2002
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                                          ABK48986;
RESULT 1
ABK48986
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Query Match
Best Local Similarity
Matches 25; Conserv
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FOXC2 polypeptide
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   misc difference
                                        misc difference
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/note= "Region coding for 5'part of alternative protein"
The invention describes an isolated human FOXC2 promoter region. The mammalian FOXC2 promoter region for the medulation of FOXC2 polypeptide expression has therapeutic value in treating type II diabetes mellitus, obesity, hypercholesterolaemia, other cardiovascular diseases or dyslipidaemias. This sequence encodes the mouse mesenchyme forkhead if (MHF-1) protein (also called FOXC2 transcription factor), described in the method of the invention
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Fragment of the FOXC2 enhancer. Specifically claimed in claim 15" 1250. .2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= e
/note= "Fragment of the FOXC2 enhancer. Specifically
claimed in claim 16"
223. .231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= h / hote= "Fragment of the FOXC2 enhancer. Specifically claimed in claim 14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= k
/note= "Fragment of the FOXC2 promoter. Specifically
claimed in claim 3"
                                                                                                                                                                                                                                                                              Transcription factor; FOXC2; antidiabetic; anorectic; antilipaemic; cardiovascular; FOXC2 potypeptide expression modulator; FOXC2 promot diabetes mellitus; obesity; hypercholesterolaemia; dyslipidaemia; cardiovascular disease; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enhancer. Specifically
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/note= "First exon according to the alternative
transcript"
1...186
                                                                           Sequence 6021 BP; 1350 A; 1675 C; 1642 G; 1354 T; 0 U; 0 Other;
                                                                                                                  ö
                                                                                               100.0%; Score 25; DB 6; Length 6021; 100.0%; Pred. No. 0.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= d
note= "Alternative first exon splice site"
116. .475
                                                                                                                 0; Indels
                                                                                                                                                                                                                                                             Genomic DNA encoding human transcription factor FOXC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Fragment of the FOXC2 claimed in claim 12" 359. .375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= g
/note= "Fragment of the FOXC2
claimed in claim 13"
                                                                                                                  Mismatches
                                                                                                                                                      cadriccacaaraaacaaacrercc 382
                                                                                                                                   1 CAGTCCACAATAAACAAACTGTCC 25
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .215
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                                                                                                                                                                                                     BP
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                                                                                                                 Conservative
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                                                                                                      Best Local Similarity
Matches 25, Conserv
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                                                                                                                                                                                                                                          02-JUL-2002
                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_signal
                                                                                                                                                                                                                      ABK48984;
                                                                                                                                                       358
                                                                                               Query Match
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note= "First exon according to the published form of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter region that modulates the expression of a is useful for treating obesity and type II diabetes
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                     Specifically
                                                                                                             Specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= q
note= "Portion of polypeptide used in alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alternative
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note= "Region coding for DNA-binding domain"
516. .4629
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/*tag= j
claimed in claim 2"
1692. 1703
//tag= "Fragment of the FOXC2 promoter.
//note= "Fragment of the FOXC2 promoter.
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note= "Second exon according
                                                                                                                                                                                                                                                                                                                                                      note= "Transcription factor"
448. .2735
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                                                                                                                                                                                                                                                                                                                                          product= "FOXC2"
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10-OCT-2000; 2000US-0238897P.
09-NOV-2000; 2000SE-00004102.
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2516. .3740
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3741. .4629
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235. .3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOV-) BIOVITRUM AB
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RESULT 3

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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also concluded is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for inforensics, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is useful as a down/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly and printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polymucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                 Human, ss, sequencing by hybridisation, SBH, expressed sequence tag; genome mapping, biodiversity, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones LW
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Pred. No. 2.4e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seqdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 26403; 44pp; English
                            13970 ATTCCACAATATATACAACTATCC 13993
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25
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90.98;
                                                                                                     ACH39191
ID ACH39191 standard; cDNA; 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                Human foetal brain cDNA #558
                                                                                                                                                                                             13-OCT-2003 (first entry)
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IABAT I.
) STACHE-CRAIN B
//) DICKSON M C.
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                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                           ACH39191;
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(STAC/)
(DICK/)
(JONE/)
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                                                                                      RESULT 5
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1 LOCUS ABQ84281 Accession Abg84281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method (MI) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            t t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
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                                                                                                                                                           Plant; bacterial infection; fungal infection; viral infection; rice;
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T, Zou
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                                                                                                                                                                                                                                                                                                                                                                                                                                Goff SA, Hora Z, Zhu T,
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Whitham S, Xie Z,
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Pred. No. 2.5e+02;
); Mismatches 3;
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210000
310000
410000
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fragments
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S, Tao Y,
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91.3%;
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nilarity 87.5%;
Conservative
                 ADA72007 standard; DNA; 1019
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200001
300001
400001
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                                                                                      (first entry)
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es 21; Conservative
                                                                                                                        Rice gene, SEQ ID 5332
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ABQ84281_0
ABQ84281_1
ABQ84281_2
ABQ84281_3
ABQ84281_3
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ABQ84281.1
WP Sequence split.ii
WP ABQ84281.0
WP ABQ84281.1
WP ABQ84281.2
WP ABQ84281.2
WP ABQ84281.3
WP ABQ84281.3
                                                                                                                                                                                                                   Oryza sativa
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Katagiri F,
                                                                                      20-NOV-2003
                                                                                                                                                                                                                                                                                        03-JAN-2003
                                                   ADA72007;
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Best Local
                                                                                                                                                                              gene; ds.
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   ADA72007
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Gaps

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(first entry)

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The present sequence encodes a human transmembrane protein. The specification describes transmembrane proteins designated KIAA0880, 65h2 and 593. The proteins and polymucleotides can be used for screening assays, detection assays, e.g. chromosome mapping, tissue typing, forensic biology and predictive medicine, e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics. They polymucleotides can also be used for the recombinant production of 65h2 and 533 proteins, which can be used in assays to detect compounds which modulate their activity. These compounds are useful in the treatment of diseases characterized by aberrant activity or expression of protein which catalyse or facilitate transport of charged organic compound, e.g. prostaglandins and thromboxanes
                                                                                                                                                                                                     Human, transmembrane protein, 65h2 protein, 593 protein, prostaglandin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecules encoding transmembrane proteins designated 65h2 and 293 are useful for screening assays, detection assays and in
                                                                                                                                                    Nucleotide sequence of a human transmembrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 181-194; 215pp; English.
                                                                                                                                                                                                                              thromboxane, KIAA0880 protein; ss
AAF54867 standard; DNA; 50000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000; 2000WO-US020521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-1999; 99US-00365162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-138648/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65h2 and 293 are use
predictive medicine.
                                                                                                                                                                                                                                                                                                                                WO200109185-A2.
                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2001.
                                                                                               15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curtis RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF54868;
                                                    AAF54867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF54868/C
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50811, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The mucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for information expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations in forences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of corticular for generating antisense DNA or RNA. The present sequence is useful for generating antiscase specific for it. The present sequence is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. Huml?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                             Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; BST; genome mapping; biodiversity; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 464 BP; 135 A; 98 C; 109 G; 116 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 75.2%; Score 18.8; DB 8; Best Local Similarity 90.9%; Pred. No. 2.4e+02; Matches 20; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 27704; 44pp; English.
                                                                                                        ACH40492 standard; cDNA; 464 BP.
                                                                                                                                                                                                                                                            Human foetal brain cDNA #1859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2001; 2001US-00918995.
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                                                                                                                                                                                                          (first entry)
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LABAT I.
STACHE-CRAIN B.
DICKSON M C.
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(LABA/) LABAT I.
(STACK) STACKE-CRAIN
(DICK/) DICKSON M C.
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-615964/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                        JS2003073623-A1
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                          13-OCT-2003
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                                                                                                                                                         ACH40492;
                                                    RESULT 6
ACH40492
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                                                                                                                                                                                                                                                                                                                                                  Human, transmembrane protein, 65h2 protein, 593 protein, prostaglandin,
thromboxane, KIAA0880 protein, ss.
                                                                  Gaps
Sequence 50000 BP; 13944 A; 11451 C; 11177 G; 13428 T; 0 U; 0 Other;
                                                                  ;
0
                              Query Match

75.2%; Score 18.8; DB 4; Length 50000;
Best Local Similarity 90.9%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                       Genomic nucleotide sequence of a human 65h2 protein.
                                                                                                                                  1142 Tacacaaaaaaacaaacrerec 1121
                                                                                                  4 TCCACAAATAAACAAACTGTCC 25
                                                                                                                                                                                                                     AAF54868 standard; DNA; 81145 BP.
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200109185-A2
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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391 TACACAAAAAAAAAAAAAAAAAAAAAAAAAA 4 TCCACAAATAAACAAACTGTCC 25

à g RESULT 7 AAF54867/c

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The present sequence encodes a human transmembrane proteins designated 65h2. The specification also describes a transmembrane protein designated 593 and KIAA0880. The proteins and polynucleotides can be used for screening assays, detection assays, e.g. chromosome mapping, tissue typing, forensic biology and predictive medicine, e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics. They polynucleotides can also be used for the recombinant production of 65h2 and 593 proteins, which can be used in assays to detect compounds which diseases their activity. These compounds are useful in the treatment of diseases characterized by aberman activity or expression of protein which catalyse or facilitate transport of charged organic compound, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice endosperm expression sequence label and genechip prepared from it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice; endosperm expression sequence label; gene chip; babel technique;
                                                                                                                                                                                                     New nucleic acid molecules encoding transmembrane proteins designated 65h2 and 293 are useful for screening assays, detection assays and in predictive medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 81145 BP; 22396 A; 18624 C; 18484 G; 21641 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.2%; Score 18.8; DB 4; Length 81145; 90.9%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice endosperm expression sequence label #23.
                                                                                                                                                                                                                                                                     Disclosure, Fig 1L1-1L36, 215pp, English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 TCCACAAATAAACAAACTGTCC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostaglandins and thromboxanes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2001; 2001CN-00135874.
                                               28-JUL-2000; 2000WO-US020521
                                                                             99US-00365162
                                                                                                          (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2001; 2001CN-00135874
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Best Local Similarity 90.9
Matches 20; Conservative
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                                                                             30-JUL-1999;
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                08-FEB-2001
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                                                                                                                                            Curtis
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                                         The invention describes a novel rice endosperm expression sequence label and the gene chip formed from it. The expression sequence babel technique is used to create a rice endosperm cDNA library. Non-redundant expression sequence labels are then combined and used to create a gene chip by microarray techniques. This sequence represents a rice endosperm expression sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid comprising any one of
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                        ch 74.4%; Score 18.6; DB 7; Length 494; 1 Similarity 84.0%; Pred. No. 2.9e+02; 21; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                          Sequence 494 BP; 132 A; 117 C; 102 G; 143 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL,
Forsyth RA,
                 Claim 1; Page 18 (Disclosure); 29pp; Chinese.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; SEQ ID NO 22176; 1766pp; English.
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                                                                                                                                                                                                                                                                                1 CAGTCCACAAATAAACAAACTGTCC 25
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Carr GJ,
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06-SEP-2001, 2001US-00948993.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-0362269P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2002; 2002WO-US009107
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Trawick JD,
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                                                                                                                                                                                                                             Best Local Similarity
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Wall D,
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the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts, (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or product is oversxpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for required for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target or proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target or for electronic format directly from WIPO at the was obtained in cells cher, why wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 3.7e+02;
0; Mismatches 1; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 816 BP; 255 A; 137 C; 172 G; 252 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACAATAAACAAACTTTC 520
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 95...
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
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ContinuaTion (10 of 19) of AAT42063 from base 900001 (Haemophilus influenzae complete gf WP Sequence split into 19 fragments LOCUS AAT42063 Accession Aat42063
WP AAT42063—01 100001 100000
WP AAT42063—02 200001 210000
WP AAT42063—04 400001 210000
WP AAT42063—05 500001 510000
WP AAT42063—06 600001 510000
WP AAT42063—07 7100000
WP AAT42063—09 900001 1010000
WP AAT42063—10 1000001 1110000
WP AAT42063—11 1100001 1110000
WP AAT42063—12 1200001 1110000
WP AAT42063—13 1200001 1110000
WP AAT42063—14 100001 1110000
WP AAT42063—15 1400001 1510000
WP AAT42063—16 1600001 1710000
WP AAT42063—16 1600001 1710000
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AAT42063_10
Continuation (11 of 19) of AAT42063 from base 1000001 (Haemophilus influenzae complete 9
WP Sequence split into 19 fragments LOCUS AAT42063 Accession Aat42063
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discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                 Gaps
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                                                                                      Sequence 6347 BP; 1734 A; 1346 C; 1299 G; 1968 T; 0 U; 0 Other;
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                                                                                                                 73.6%; Score 18.4; DB 4; Length 6347; 95.0%; Pred. No. 4.3e+02; ive 0; Mismatches 1; Indels 0.
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Pred. No. 5.4e+02;
); Mismatches 1;
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                                                                                                                                                                             1 CAGTCCACAAATAAACAAAC 20
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95.0%;
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                                                                                                                     Query Match
Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                      AAT42063_09
Continuation (10 of 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fragment Name
AAT42063 00
AAT42063 01
AAT42063 02
AAT42063 03
AAT42063 05
AAT42063 06
AAT42063 06
AAT42063 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid array containing Xenopus embryonic nucleic acids is useful to identify genes involved in embryonic development, to identify different types of embryonic cells, and to diagnose developmental
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Frog, ss; embryonic development; developmental disorder; microarray; cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation. This would be useful for diagnosing developmental disorders and for identifying different types of embryonic cells. The present sequence is one of the 770 Xenopus embryonic CDNA sequences
                                                                                                  ;
0
                                                         Length 110000;
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llarity 87.0%; Pred. No. 4.48+02;
Conservative 0; Mismatches 3; Indels (
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                                                                                                    1; Indels
                                                       Score 18.4; DB 2;
Pred. No. 5.4e+02;
0; Mismatches 1;
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1810000
1830121
                                                                                                                                                                         5260 CCACAATAAACAAACTTTC 5279
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                                                                                                                                           5 CCACAAATAAACAAACTGTC 24
                                                                                                                                                                                                                                                                                  ABS77078 standard; cDNA; 686 BP
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1700001
                                                            Query Match 73.6%;
Best Local Similarity 95.0%;
Matches 19; Conservative
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Best Local Similarity
Matches 20; Conserv
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AAT42063_17
AAT42063_18
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Gaps

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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30694.
                                                                                         Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
         345 CAGTCCACAATGACCAAACGGT 323
1 CAGTCCACAATAAACAAACTGT 23
                                                                                                                                                  17-JAN-2001; 2001WO-US001354.
                                                                                                                                                                                                                                                                                              000US-0225214P
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0231243P
                                          AAK75882 standard; DNA; 5124
                                                                 07-NOV-2001 (first entry)
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06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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                                                     AAK75882;
                             RESULT 15
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2000US-0246475P.
2000US-0246476P.
2000US-0246477P.
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AANSA951 to AANS4702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

activity, and can be used in gene therapy and vaccine production. (I)

cytoteins and polynuclectides may be used in the prevention, diagnosis and

cxample, they may be used to treat disorders associated with decreased

example, they may be used to treat disorders associated with decreased

cxample, they may be used to treat disorders associated with decreased

cxample the activity of (I) by expressing inactive proteins or to

that affect the activity of (I) by expressing inactive proteins or to

cyphynuclectides may be used to product of (I). Additionally, by inserting the

cyphynuclectides may be used to produce the secreted (I), by inserting the

cyphynuclectides may be used to produce the secreted (I), by inserting the

cyphynuclectides may be used to produce the secreted (I), by inserting the

cyctein. (I) proteins and polynucleotides may be used to prevent,

ciagnose and treat immune/haematopoietic-related diseases, especially

cancers and cancer metastases of haematopoietic antigen genomic

to AANS964 represent tuman immune/haematopoietic antigen genomic

sequences from the present invention. AAANS4921 to AAXS4950 and AAM82169

crepresent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 30694; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5124 BP; 1322 A; 1253 C; 1083 G; 1466 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Barash SC, Ruben SM
                                   2000US-0249299P.
2000US-0250160P.
2000US-0250160P.
2000US-0250391P.
2000US-0251330P.
2000US-0251988P.
                                                                                                                                                                 2000US-0256719P.
2000US-0251479P.
2000US-0251856P.
                                                                                                                                                                                                                                                                             2000US-0251989P
2000US-0251990P
                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483426/52.
                                                                                               01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
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Search completed: March 25, 2004, 10:25:20 Job time : 29.9441 secs

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Sequence 1, Appli
Sequence 22, Appl
Sequence 24, Appl
Sequence 1426, Ap
Sequence 2355, Ap
Sequence 2355, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                                                                            Sequence 11, Appl
Sequence 11, Appl
Sequence 54, Appl
Sequence 2101, Ap
Sequence 1803, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 32, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-09-557-884-1
i Sequence 1, Application US/09557884
j Patent No. 1650581
i GENERAL INFORMATION:
j APPLICANT: Fleischmann et al.
i TITLE OF INVENTION: The Nucleotide sequence of
TITLE OF INVENTION: The nucleotide sequence of
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 1830121;
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                  US-09-319-056B-22
US-09-319-056B-24
US-09-107-532A-2355
US-09-134-000-135
US-09-23-134-1
US-08-922-801-1
US-08-922-801-1
US-08-557-884-1
US-09-557-884-1
US-09-557-884-1
US-09-557-884-1
US-09-134-000C-2101
US-09-134-000C-2101
US-09-134-000C-2101
US-09-134-000C-2101
US-09-134-000C-2101
US-09-134-000C-2101
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US-09-134-000C-2101
US-09-134-000C-2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: I
CORRESSEONDERS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READALE FORM:

MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Fentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-APT-2000
CLASSIPICATION: vINKNOWN>
PRIOR APPLICATION: vINKNOWN>
PRIOR APPLICATION: vINKNOWN>
APPLICATION NUMBER: 08/476,102
FILING DATE: UNFORMATION:
NAME: MICHAEL S. MARKS
REGISTRATION NUMBER: 41,971
REPERRENCE/DOCKET NUMBER: PB186F3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8639
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LIENGTH: UNDER EASTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.6%; Score 18.4; L
Best Local Similarity 95.0%; Pred. No. 76;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 CCACAAATAAACAAACTGTC 24
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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Sequence 195, App
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Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
                                                                                                                                  March 25, 2004, 09:55:14 ; Search time 4.91739 Seconds (without alignments) 2821.370 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1
Sequence 1
Sequence 7
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued Patents NA:*
1: /cgn2_6/ptodate/2/ina/5A_COMB.seq:*
    /cgn2_6/ptodate/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/FCTUG COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUG COMB.seq:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     682709 segs, 277475446 residues
                                                                                                                                                                                                                                                           1 cagtccacaaataaacaaactgtcc 25
                                                                                                                                                                                                            US-09-963-285-1_COPY_378_402
25
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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70.4 1056 4
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Match Length DB
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65.6
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Perfect score:
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                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                       Searched:
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US-09-543-681A-2690

Sequence 2690, Application US/09543681A

Sequence 2690, Application US/09543681A

Sequence 2690, Application US/09543681A

Sequence 2690, Application US/0909

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: DIGGEOUS AND THERAPEUTICS

TITLE OF INVENTION: DIGGEOUS

TITLE OF INVENTION: DIGGEOUS

TITLE OF INVENTION: DIGGEOUS

TITLE OF INVENTION: DIGGEOUS

TITLE OF INVENTION: DIGGEOUS

TITLE OF INVENTION: DIGGEOUS

TITLE OF INVENTION: DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 2690

LENGTH: 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-221-017B-971

Sequence 971, Application US/09221017B

Patent No. 6444799

GENERAL INFORMATION:

APPLICANT: ROSS, Bruce C.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF

OCRESPONDENCES: 1120

CORRESPONDENCE ADDRESS:

ADDRESSE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: GA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

SOFTWARE: FSEUSED for Windows

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1056;
                                                                                                                                                                                                                                                                                                                                             Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                           ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700548714H1
US-09-313-294A-195
                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.6; DE Pred. No. 76; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                          Score 17.6; DE Pred. No. 65; 0; Mismatches
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 195
LENGTH: 281
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 CAATCCACAGAGAACAAACTCTC 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Proteus mirabilis
US-09-543-681A-2690
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                           FEATURE
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Sequence 195, Application US/09313294A
Sequence 195, Application US/09313294A
Septent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Laura Y.
APPLICANT: Sherman, Baradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
                                                                                                                                                                                                                                                                                 Hamilton O. Smith
J. Craig Venter
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 1830121;
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                                                                                                                                                                                                                                                                                                                                                                                              Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville, STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug_2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/ACENT INFORMATION:
REGISTRATION NUMBER: 40,302
REGISTRATION NUMBER: 40,302
REGISTRATION NUMBER: 40,302
REGISTRATION NUMBER: 40,302
REGISTRATION NUMBER: 40,302
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95.0%; Pred. No. 76;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOPTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1005260 CCACAAATAAACAAACTTTC 1005279
     1005260 CCACAAATAAACAAACTITC 1005279
                                                                                                                                                                                                                 APPLICANT Robert D. Fleischmann
Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 310-309-8439
INPORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
                                                                                                                                              Sequence 1, Application US/09643990A, Patent No. 6528289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 CCACAAATAAACAAACTGTC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                       RESULT 2
US-09-643-990A-1
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Sequence 110, Application US/09157177

Sequence 110, Application US/09157177

Parent No. 6090558

GENERAL INFORMATION:
APPLICANT: Butler, John M.
APPLICANT: Butler, John M.
APPLICANT: Hi, Jate, Joseph A.
APPLICANT: Becker, Christopher H.
ITILE OF INVENTION: REPERAT MARKERS
ITILE OF INVENTION: REPERAT MARKERS
ITILE OF INVENTION: REPERAT MARKERS
CURRENT APPLICATION NUMBER: US/09/157,177

CURRENT PILING DATE: 1998-09-18

SEALIER APPLICATION NUMBER: 60/059,415

SEALIER PILING DATE: 1997-09-19

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                        Sequence 3, Application US/10254869

Retent No. 6653117

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMY: Ex. Jame et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO11601V
CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
NUMBER: OSEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
ILBUTCH: 148567
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                    Indels
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 4;
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                                                                                                                     87125 CATTACACAGATAAAGAACTGTC 87148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGTCCACAATAAACAAACTGTC 24
                                                                      1 CAGTCCACAATAAACAAACTGTC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature; LCCATION: (1)...(148567); OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 94.7%;
Matches 18; Conservative
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US-09-157-177-110/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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Patent No. 6492155

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: TACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE REFERENCE: CL001160

CURRENT APPLICATION NUMBER: US/09/801,876B

CURRENT PILLING DATE: 2001-03-09

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FactSeQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 148667
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Best Local Similarity 83.3%; Pred. No. 89;
Matches 20; Conservative 0; Mismatches
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                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION NUMBER: PCT/AU98/01023
ATTORNEY/AGENT: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1187 CAGTCCACAAACAAACGAATAGTC 1210
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAGTCCACAATAAACAAACTGTC 24
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LOCATION: (1)...(148567)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                            NAME: MONTOY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-6600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ ID NO: 971:
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 1...3615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-801-876B-3
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Sequence 17. Application US/09319588C

Patent NO. 6509018

Patent NO. 6509018

GENERAL INFORMATION:
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INSERM
APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS
APPLICANT: MAUCIERE, PHILIPPE
APPLICANT: MAUCIERE, PHILIPPE
APPLICANT: SIMON Francoise
APPLICANT: SIMON Francoise
APPLICANT: SARRE-SINOUSSI, Francoise
APPLICANT: SARRE-SINOUSSI, Francoise
APPLICANT: BARRE-SINOUSSI, Francoise
APPLICANT: BARRE-SINOUSSI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOISI, PRANCOI
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68.8%; Score 17.2; DB 4;
Best Local Similarity 86.4%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GTCCACAAATAAACAAACTGTC 24
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 9183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.4
Matches 19; Conservative
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; LOCATION: (1)
US-09-319-588C-17
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                                                                                                Sequence 15, Application US/09446301A
Sequence 15, Application US/09446301A
Patent No. 6506893
GENERAL INFORMATION:
APPLICANT: EL SOLH
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: 1999-12-20
GURRENT FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 51
SSETWARE: PATENT VEY: 2.1
SSEQ ID NO 15
LENGTH: 2411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: E1 Solh, Nevine

APPLICANT: E1 Solh, Nevine

APPLICANT: E1 Solh, Nevine

TITLE OF INVENTION: POLYNUCLECTIDES AND THEIR USE FOR DETECTING RESISTANCE

TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED

TITLE OF INVENTION: COMPOUNDS

TITLE OF INVENTION: COMPOUNDS

TITLE OF INVENTION: US/09/099,932

CURRENT APPLICATION NUMBER: US/09/099,932

CURRENT APPLICATION NUMBER: 60/050,380

EARLIER APPLICATION NUMBER: 60/050,380

SARLIER PILING DATE: 1997-06-20

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 47

LENGTH: 2411
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Pred. No. 1e+02;
0; Mismatches 1; Indels 0
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Patent No. 6570001
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; LOCATION: (700..2355, 2388..2411)
US-09-446-301A-15
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Best Local Similarity 94.7%;
Matches 18; Conservative
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; LOCATION: (2388)..(2411)
US-09-099-932-47
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LOCATION: (700)..(2355)
                                                  RESULT 9
US-09-446-301A-15/c
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US-09-099-932-47/c
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Length 2559;

3; Indels

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APPLICANT: INSTITUT PASTEUR
APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS
APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS
APPLICANT: INSTITUT PASTEUR
APPLICANT: INSTITUT PASTEUR
APPLICANT: IOUSSERT-AJAKA, Ibtissam
APPLICANT: SIMON, Francoise
APPLICANT: SARAGOSTI, Sentob
APPLICANT: SARAGOSTI, Sentob
APPLICANT: SARAGOSTI, Sentob
APPLICANT: SARAGOSTI, Sentob
APPLICANT: SARAGOSTI, Sentob
APPLICANT: SARAGOSTI, Sentob
APPLICANT: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATIONS.
FILE REPERBNCE: 598US12
CURRENT APPLICATION NUMBER: US/09/319,588C
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: FR96/15087
PRIOR PILING DATE: 1996-12-09
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1247 Grecacaarrracaarcrere 1226
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                                                                                                                                                        Sequence 1, Application US/09319588C Patent No. 6509018
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RESULT 11

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NAME/KEY: misc feature
LOCATION: (270501)..(285000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (285501)..(300000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (300501)..(31500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (315001)..(333000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (315001)..(345000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (345001)..(345000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (345001)..(375000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (345001)..(455000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (345001)..(450000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (435001)..(450000)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (435001)..(525000)
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NAME/KEY: misc feature
LOCATION: (435001)..(525000)
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NAME/KEY: misc feature
LOCATION: (4350001)..(350000)
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NAME/KEY: misc feature
LOCATION: (4350001)..(350000)
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LOCATION: (615501)..(63000)
OCHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
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LOCATION: (570001)..(585000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (585001)..(600000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g
                             RESULT 13
US-09-198-452A-1
Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: GTIffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering Prints of INVENTION: and treatment of infection
TITLE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
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LOCATION: (210001)..(225000)
OTHER INPORMATION: n=a or or g or t
NAME/KEY: misc feature
LOCATION: (225001)..(24000)
OTHER INPORMATION: n=a or or g or t
NAME/KEY: misc feature
LOCATION: (240001)..(255000)
OTHER INPORMATION: n=a or or g or t
OTHER INPORMATION: n=a or or g or t
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LOCATION: (45001)..(60000)
OTHER INFORMATION: nea or c or g or t
NAME/KEY: misc feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: nea or c or g or t
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
LOCATION: (30001)...(45000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g
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ORGANIGM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(15000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
LOCATION: (15001)...(30000)
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAF TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709. 2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ. ID NOS: 3840
LENGTH: 438
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Sequence 1109, Application US/09833381

Patent No. 6672186

GENERAL INFORMATION:

TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs

TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs

TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs

TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs

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TITLE OF INVENTION: NO. 6672186e1 Nucleic Acid and Protein Homologs

TITLE OF INVENTION: NO. 6672186e1 Nucleic Acid and Protein Homologs

TITLE OF INVENTION: NO. 6672186e1 Nucleic Acid Acid Acid Acid
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Pred. No. 1.2e+02;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 cadrictroaaaraaccracrarisc 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 cagrccaaraacaaacaaaarggcc 168
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; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-476
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US-09-833-381-1109/c
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LOCATION: (85501)..(87000)
OTHER INFORMATION: n=a or or gor t
NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (88501)..(90000)
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (75001)...(75000)
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (75001)...(78000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (79501)...(79500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (79501)...(81000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (82500)
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LOCATION: (82500)
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LOCATION: (90001)...(915000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
CCCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (720001)..(735000)
THERE INFORMATION: n=a or c or g or
AAME/KEY: misc_feature
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0; Gaps

Query Match 68.8%; Score 17.2; DB 4; Length 1230025; Best Local Similarity 86.4%; Pred. No. 2e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0;

447969 rccacaacraaacgagcrercc 447990

4 TCCACAAATAAACAAACTGTCC 25

à

Sequence 476, Application US/09540236; Patent No. 6673910; GENEAL INFORMATION: APPLICANT: Gary L. Breton et al.

RESULT 14 US-09-540-236-476/c

Sequence 1095, Ap Sequence 11869, Ap Sequence 118026, Ap Sequence 118026, Sequence 317, App Sequence 3169, A Sequence 3169, A Sequence 228785, Sequence 229330, Sequence 229331, Sequence 259331, Sequence 3241, A Sequence 3241, A Sequence 3242, A Sequence 357, App Sequence 357, App Sequence 357, App Sequence 357, App Sequence 357, App

Sequence 3, Appli Sequence 3, Appli Sequence 2767, Ap Sequence 2767, Ap Sequence 3094, Ap

Sequence 1055, Ap Sequence 81, Appl Sequence 3, Appli

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100.0%; Score 25; DB 9; Length 6021; 100.0%; Pred. No. 0.67; rative 0; Mismatches 0; Indels (
15 US-10-227-577-1494
15 US-10-292-798-1095
15 US-10-292-798-1369
15 US-10-292-798-1369
15 US-10-292-798-1369
15 US-10-227-678-1369
15 US-10-227-678-218026
15 US-10-227-678-231669
15 US-10-027-632-36169
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18 US-10-27-632-259331
19 US-10-27-632-259331
19 US-10-425-114-3532
19 US-09-966-880A-9
19 US-09-966-880A-9
19 US-09-966-880A-9
19 US-09-966-880A-9
19 US-09-968-80B-9
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11 US-10-254-869-3
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11 US-10-253-904-15
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US-09-963-285-5
Sequence 5, Application US/09961285
Sequence 5, Application US/09961285
Sequence 6, Application US/09961285
Sequence 6, Application US/09961285
Sequence 7
GENERAL INFORMATION:
APPLICANT: Enerbock, Katarina APPLICANT: Rondahl, Lena APPLICANT: Rondahl, Lena APPLICANT: Rasserman, Wyeth TILLE OF INVENTION: PROMOTER SEQUENCES FILE REFERENCE: 13425-042001
CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2000-10-0-26
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
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Matches 25; Conservative
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ORGANISM: Mus musculus
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LENGTH: 6021
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Sequence 1, Appli
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(cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

(cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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15 US-10-027-632-53-50

10 US-09-918-995-26403

10 US-09-918-995-27404

13 US-10-063-763-4

14 US-10-063-763-4

15 US-10-067-763-4

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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Best Local Similarity 87.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Sequence 286, Application US/10085117 | Sequence 286, Application US/10085117 | Publication No. US2003232334A1 | GENERAL INFORMATION: APPLICANT: Morfis, David W. | APPLICANT: Morfis, David W. | TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER | TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER | FILE REFERENCE: 259452000121 | CURRENT APPLICATION NUMBER: US/10/085,117 | CURRENT FILING DATE: 2002-02-27 | PRIOR APPLICATION NUMBER: US 09/798,586 | PRIOR APPLICATION NUMBER: US 09/798,586 | PRIOR PRIOR FILING DATE: 2001-03-02 | NUMBER OF SEQ ID NOS: 361 | SOFUMBER PRESEQ for Windows Version 4.0 | SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUMBER OF SEQ ID NO 286 | MINDOWS NUM
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                                                                                                                                                             DB 15; Length 1907;
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publication No. US20030073623A1
publication No. US20030073623A1
general information:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PSESEQ for Windows Version 3.0
LENGTH: 455
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80.8%; Score 20.2; I

Best Local Similarity 88.0%; Pred. No. 62;

Matches 22; Conservative 0; Mismatches
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CCATION: (1)...(455)
OTHER INFORMATION: n = A,T,C or G
US-09-918-955-26403
; LOCATION: (1)...(1907)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-53050
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Best Local Similarity 90.99
Matches 20; Conservative
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CRGANISM: Homo sapiens
US-10-085-117-286
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US-09-918-995-26403
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; Bublication No. US20030204075A9
; Publication No. US20030204075A9
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REFERENCE: 108927.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-09-8
; PRIOR FILING DATE: 1999-09-8
; PRIOR FILING DATE: 1999-09-8
; PRIOR FILING DATE: 1999-09-8
; PRIOR FILING DATE: 1999-09-8
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-08-09
; ROOTHWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 53050
; LENGTH: 1907
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Best Local Similarity 100.0%; Score 25; DB 9; Length 6458;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                             US-09-963-285.
US-09-963-285.
Sequence 1. Application US/09963285
Patent No. US2002009707A1
GENERAL INFORMATION:
APPLICANT: Enerbck, Sven
APPLICANT: Krook, Katarina
APPLICANT: Rondahl, Lena
APPLICANT: Rondahl, Lena
APPLICANT: Wasserman, Wyeth
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFREENCE: 134.25-04.201.
FILE PREPARENT PLING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0003435-5
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 1
SEQ ID NO 1
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; LOCATION: (2235)...(3737)
US-09-963-285-1
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ORGANISM: Homo sapiens
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ORGANISM; Human
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US-10-027-632-53050
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TITLE OF INVENTION: No. US20030022286Alel Transporter-Like Genes and Uses Therefor FILE REFERENCE: 10147-8
CURRENT APPLICATION NUMBER: US/10/060,763
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 50000
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Sequence 2550, Application US/10027632

Publication No. US2030204075A9

GENERAL INFORMATION:

APPLICANT' Wang David G.

TITLE OF INVENTION: Telegation and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: POLYMORER: US 60/218,006

PRIOR FILING DATE: 2002-04-30

PRIOR PAPLICATION NUMBER: US 60/198,676

PRIOR PAPLICATION NUMBER: US 60/198,676

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 1999-04-20

PRIOR PELING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-09-08-08

PRIOR FILING DATE: 1999-09-08-08

PRIOR PRIING DATE: 1999-09-08-09

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PRIOR PRIOR PRIECE 1999-09-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: PRACTH. 437
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Pred. No. 4.6e+02;
0; Mismatches 2;
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Chery1
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
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Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                                                                                                                        TYPE: DNA; ORGANISM: Homo sapiens US-10-060-763-4
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US-10-282-122A-22176/c
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-10-027-632-2550
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US-310-063-763-4/c

Sequence 4, Application US/10063763

Sequence 10 No. US2010001663A1

SEQUENCE 10 NO. US2010001663A1

APPLICANT: CURTIS, Rory A.J.

TITLE OF INVENTION:

PILE REPRENCE: 10147-8

CURRENT APPLICATION NUMBER: US/10/063,763

CURRENT FILING DATE: 1999-UGL-30

PRIOR FILING DATE: 1999-UGL-30

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 464;
                                                                                                                                                                                                                                    APPLICANT: Hyeeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT RELIGHED ATE: 2001-07-30
PRIOR PELICATION NUMBER: US/09/215,076
PRIOR FILING DATE: 1999-01-20
NUMBER: OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.2%; Score 18.8; DB 10; Best Local Similarity 90.9%; Pred. No. 1.9e+02; Matches 20; Conservative 0; Mismatches 2;
                                                                                                                                                                 Sequence 27704, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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                       376 TACACAAAAAAACAAACTGTCC 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.9
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Curtis, Rory A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-063-763-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(464)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                              US-09-918-995-27704
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US-10-060-763-4/c
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NAME/KEY: misc feature
LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
NAME/KEY: misc_36636)
OTHER INFORMATION: n equals a,
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LOCATION: (44975)..(44975)
THER INFORMATION: n equals a,
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COCATION: (45732)..(45732)
OTHER INFORMATION: n equals a,
FEATURE:
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LOCATION: (47036)..(47036)
LHER INFORMATION: n equals a,
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a,
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LOCATION: (51602)..(51602)
JTHER INFORMATION: n equals a,
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LOCATION: (44416)..(44416)
OTHER INFORMATION: n equals a,
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OCATION: (45593)..(45593)
OTHER INFORMATION: n equals a,
AMB/KEY: misc_feature
OCATION: (4747)..(4747)
THER INFORMATION: n equals a,
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a,
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ACCATION: (36551)..(36551)
MHER INFORMATION: n equals a,
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a,
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LOCATION: (51786)..(51786)
JTHER INFORMATION: n equals
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LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals
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LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals
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LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals
FEATURE:
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US-10-329-960-1
Sequence 1, Application US/10329960
| Publication No. US2030099277A1
| GENERAL INFORMATION:
| APPLICANT: Fleischmann et al. | APPLICANT: Fleischmann et al. | APPLICANT: Fleischmann et al. | APPLICANT: Pleischmann et al. | APPLICANT: UNWERFUR: US/10/329,960 | APPLICANT: UNWERF: US 09/643,990 | APPLICANT: UNWERF: US 08/437,429 | APRIOR FILING DATE: 1995-06-07 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1995-04-21 | APRIOR FILING DATE: 1993-04-21 | APRIOR PARTIOR DATE: 1993-04-21 | APRIOR PARTIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DATE: 1993-04-21 | APRIOR DAT
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-01-03
PRIOR PLING DATE: 2000-01-03
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2001-02-09
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PRIOR PLING DATE: 2001-03-03-03-03-03-03-03-03-03-03-
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ORGANISM: Haemophilus influenzae
FBATURE:
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CRGANISM: Haemophilus influenzae
US-10-282-122A-22176
             Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 95.0
Matches 19; Conservative
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NAME/KEY: misc feature
LOCATION: (139910)..(139910)
JTHER INFORMATION: n equals a, t, g or c
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OCATION: (102696)...(102696)
THER INFORMATION: n equals a, t, g
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OCATION: (105121)..(105121)
THER INFORMATION: n equals a, t, 9
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OCATION: (119750)..(119750)
THER INFORMATION: n equals a, t,
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OCATION: (122336)..(122336)
THER INFORMATION: n equals a,
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AME/KEY: misc_feature
ACATION: (120038)..(120038)
THER INFORMATION: n equals a,
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OCATION: (117136)..(117136)
THER INFORMATION: n equals a,
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OCATION: (122167)..(122167)
THER INFORMATION: n equals a,
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OCATION: (131340)..(131340)
YTHER INFORMATION: n equals a,
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OCATION: (119924)..(119924)
THER INFORMATION: n equals a,
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OCATION: (121344)..(121344)
THER INFORMATION: n equals a,
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LOCATION: (65313)..(65313)
THER INFORMATION: n equals a,
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AAME/KEY: misc_feature
COATION: (80024).(80024)
OTHER INFORMATION: n equals a,
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OCATION: (107248)..(107248)
THER INFORMATION: n equals a,
LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a,
                                                          NAME/KEY: misc_feature
LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals a,
FEATURE:
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OCATION: (100091)..(100091)
THER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (140398)..(140398)
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LOCATION: (131360)..(131360)
THER INFORMATION: n equals
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US-10-349-6/U-1

| Sequence | Application US/10329670 |
| Publication No. US20040018503A1 |
| GENERAL INFORMATION: |
| APPLICANTE | Felsiochmann et al. |
| TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Fragratic RIE REPERENCE: PB1866P |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: Thereof, and Uses Thereof |
| TITLE OF INVENTION: UNMERR: US/09/43,990 |
| PRIOR PLILING DATE: 2000-08-23 |
| PRIOR FILING DATE: 1995-06-07 |
| PRIOR PAPLICATION NUMBER: US/08/426,787 |
| PRIOR PLING DATE: 1995-06-07 |
| PRIOR PLING DATE: 1995-04-21 |
| NUMBER OF SEQ ID NOS: 1 |
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| LENGTH: NAME OF SEQ ID NOS: 1 |
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LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals a, t, g or c
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OTHER INFORMATION: n equals a, t, g or
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NAME/KEY: misc_feature
LOCATION: (152500).(152500)
OTHER INFORMATION: n equals a, t, g
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ORGANISM: Haemophilus influenzae
FEATURE:
                                                                        NAME/KEY: misc_feature
NAME/KEY: misc_feature
OCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t,
FRATURE:
NAME/KEY: misc_feature
LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a, t,
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LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (147197)...(147197)
OTHER INFORMATION: n equals a,
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LOCATION: (150841)...(150841)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc_feature
LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (152530)..(152530)
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (40808)..(40810)
OTHER:INFORMATION: n equals a, t, g or
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LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a, t, g
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LOCATION: (65309)..(65309)
OCHER INFORMATION: n equals a, t, g
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NAME/KEY: misc_feature
LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a, t,
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LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a, t,
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LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (51602)..(51602)
OTHER_INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (55369) .. (55369)
OTHER INFORMATION: n equals a,
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LOCATION: (45732)..(45732)
DTHER INFORMATION: n equals a,
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a,
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LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a,
FEATURE:
NAME/KEY: misc feature
LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (29298).
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (36543)
OTHER INFORMATION: n equals a,
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a,
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LOCATION: (44416)...(44416)
DTHER INFORMATION: n equals a,
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a, t, g or
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NAME/KEY: misc_feature
LOCATION: (131360)...(131360)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals a, t,
FEATURE:
NAME/KEY: misc_feature
LOCATION: (121344).
OTHER INFORMATION: n equals a, t,
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (122167).(122167)
OTHER INFORMATION: n equals a,
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a,
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LOCATION: (119524)..(119924)
OTHER INFORMATION: n equals a,
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LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals a,
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals a,
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LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
LOCATION: (65313)...(65313)
OTHER INFORMATION: n equals a,
FEATURE:
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals a,
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals a,
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals
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87.0%; Pred. No. 7.7e+02;
tive 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                           Length 32183;
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FAPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC007C1; CURRENT FELLING DATE: 2002-03-07; NUMBER OF SEQ ID NOS: 2442; Prior Application removed - See File Wrapper or Palm; SCPTWARE: PatentIn Ver. 2.0; SEQ ID NO 1494; LENGTH: 32183
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Frior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1494
LENGTH: 32183
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72.8%; Score 18.2; DB 9;
Best Local Similarity 87.0%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 3;
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Job time : 26.6562 secs
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Best Local Similarity 87.0
Matches 20; Conservative
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CORGANISM: Homo sapiens
US-10-091-504-1494
                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-764-869-1494
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US-10-091-504-1494/c
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Patent No. US20020084610A1

GENERAL INFORMATION:
APPLICANT: Hermati-Erivanlou, Ali
APPLICANT: Altuman, Curtis
TILLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
TILLE OF INVENTION WIMBER: US/09/910,943

CURRENT APPLICATION WIMBER: 2001-07-23

NUMBER OF SEQ ID NOS: 742

SEQ ID NO 313

LENGTH: 686
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Best Local Similarity 95.0%; Pred. No. 9.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; G
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             LOCATION: (145058)..(145058)
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NAME/KEY: misc_feature
LOCATION: (152500). (152500)
OTHER INFORMATION: n equals a, t,
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LOCATION: (150841)..(150841)
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LOCATION: (145171)...(145171)
OCHER INFORMATION: n equals a,
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NAME/KEY: misc feature
LOCATION: (147197)
OTHER INFORMATION: n equals a,
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LOCATION: (145942) ..(145942)
OTHER INFORMATION: n equals a,
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LOCATION: (152530)..(152530)
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US-09-910-943-313/c
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Length 686; 3; Indels

Query Match
72.8%; Score 18.2; DB 9;
Best Local Similarity 87.0%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 3;

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Sequence 1494, Application US/09764869; Patent No. US20020061521A1 GENERAL INFORMATION: APPLICANT: Rosen et al.

RESULT 14 US-09-764-869-1494/c

NAME/KEY: misc_feature
. LOCATION: (1)..(686)
. CTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-313

ORGANISM: Xenopus laevis

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March 25, 2004, .08:39:03 ; Search time 170.338 Seconds (without alignments) 6361.316 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID . Description	Score March Dength DB 1D	1 25 100.0 6021 10 MMMFHBAD1 Y08222 2 25 100.0 168656 9 AC009108 AC009108	3 25 100.0 178416 10 AC127554 ACI ACI ACI ACI ACI ACI ACI ACI ACI ACI	21.4 85.6 162337 2 AC101961 AC101961 Mus mus	5 20.8 83.2 202972 10 AL663052	20.4 81.6 166829 2 ACLM6300 ACLM6300 Daile 10	20.2 80.8 222745 2 AC127100 AC127100 Rattus	19.8 79.2 1019 6 AX655462 Sequenc	19.8 79.2 2993 8 AF391109 AF391109	19.8 /9.2 26845 2 ACLIGSI4 ACLIGSE ACLIGSE ACLIGSE ACLIGSE ACLISES ACL	13 19.8 .79.2 100849 9 HUMNEUROF	19.8 79.2 113200 9 AC134669 AC134669	15 19,8 79.2 139503 2 AP005289 AP005289	16 19.8 79.2 160515 9 AC135724 AC135724	19.8 79.2 187234 2 AC114142 AC114142	19 19.8 79.2 218347 2 AC126889 AC126889	19.8 79.2 297898 9 AC004526 AC004526 HOMO 8	19.4 77.6 209907 10 ACI18038 ACI18038 Mus	19.2 76.8 70313 2 AC016216 AC016216 Homo	19.2 76.8 86113 9 AF285442 ACCCCCCC ACCCCCCCCCCCCCCCCCCCCCCCCCC	19.2 /6.8 104017 9 AC105050 AC105050 AC105050 HOMO	19.2 76.8 107430 9 AC006988 AC006988 Homo	19.2 76.8 112527 9 AC012356 AC012356 Homo	29 19.2 76.8 132775 2 AC046156 AC046155 HOWG	76,8 142959 2 AC025453 AC025453 Homo	32 19.2 76.8 144264 2 AP005876 AP005876 Oryz	33 19.2 76.8 158310 2 BXZ94108 34 19.2 76 8 164376 2 ACC10823	19.2 76.8 164550 9 CNSOIRHY AL162633 Huma	36 19,2 76.8 164603 9 AC025284	19.2 76.8 169199 2 AC109292 AC109292 AC103292 AC1033407 HOMO 8	19.2 /6.6 103663 Z ACU2340/ 19.2 76 8 173829 10 AC122415 ACI22415 Mus	40 19.2 76.8 175208 10 AC112156 Mus	19.2 76.8 175577 2 AC022462 AC022462 HOMO	19.2 76.8 175749 9 ACUZ5857 ACUZ5857 ACUZ5637 ACUZ5637 ACUZ5637 ALIMAT	19.2 76.8 176267 9 AC113420 AC113420 HOMO	45 19.2 76.8 181087 10 AC125080 AC1250	ALIGNMENTS	RESULT 1	MMMFHEAD1	z	ACCESSION Y08222 VERSTON Y08222.1 GI:1869968	S mesenchyme	ORGANISM Mus musculus	
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Gaps

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Direct Submission
Submitted (27-NOV-2003) Department of Genetics, Washington
Submitted (27-NOV-2003) Department of Genetics, Wissouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 6, 2003 this sequence version replaced gi:33342444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC127554 178416 bp DNA linear ROD 27-NOV-2003
Mus musculus BAC clone RP24-323K23 from chromosome 8, complete
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4 (bases 1 to 178416)
Wilson P V
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Direct Submission
Submitted (30-UTL)
Submitted (30-UTL)-2003) Genome Sequencing Center, 4444 Forest Park
Submitted (30-UTL)-2003) Genome Sequencing Center, 4444 Forest Park
Submitted (30-UTL)-2003)
Second (30-UTL) (30-UTL)
Second (30-UTL) (30-UTL)
Second (30-UTL) (30-UTL)
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Submitted (06-AUG-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 178416)
                                                             www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
Finishing Completed at Stanford Human Genome Center and Los Alamos
Mational Laboratory
www-shgc.stanford.edv
Quality: Phrap Quality >=40 99.9% of Sequence;
Bstimated Total Number of Errors is 0.2.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 178416)
Cordes, M. and Haglund, K.
The sequence of Mus musculus BAC clone RP24-323K23
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WIGSC Web site: http://genome.wustl.edu Contact: submissions@watson.wustl.edu
Drive, Walnut Creek, CA 94598, USA
On Oct 29, 2002 this sequence version replaced gi:13786306.
Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 168656;
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                                                                                                                                                                                                        1. .168656
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3 (bases 1 to 178416)
3 (bases 1 to and Waterston, R.H. Direct Submission Submitted (17-JUL-2002) Genome Se
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Matches 25, Conservative
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                                                                                                    Mura,N.
Direct Submission
Direct Submission
Submitted (18-SEP-1996) N. Miura, Akita University School of
Submitted, Department of Biochemistry, 1-1-1 Hondo, Akita 010, JAPAN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PALPVITKVETLSPEGALQASPRSASSTPAGSPDGSLPEHHAAPNGLPGFSVETIMT
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HLHPQAPPRAQPPARAPAPAPAGATSWYLNHGGDLSHLPGHTFATQQQTPPNVREMFNS
HRLGLDNSSLGBSQVSNASCQLPYRATPSLYRHAAPYSYDCTKY"
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Unburger 1 to 168656)

Doc Joint Genome Institute.

Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Genome Institute, Stanford Human Genome Center and Los
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Direct Submission
Submitted (29-OCT-2002) DOE Joint Genome Institute, 2800 Mitchell
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1 (bases 1 to 168656)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
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Homo sapiens chromosome 16 clone RP11-46309, complete sequence.
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                                                                                                                                                                                                                                                              MAPPING INFORMATION: Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                     The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                              this
                                                                                                                                                     all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                              NOTICE: This sequence may not represent the entire insert of this folone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence is the entire insert of the clone. This clone is overlapped by ACI4170.
Location/Qualifiers
                                                                                                                                         sequence was finished as follows unless otherwise noted:
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/note="CpG island (%GC=69.2, o/e=0.78, #CpGs=269)"
[648. .16980
'rpt, family="MIR"
8383. .1840^4
   Center project name: M BB0323K23
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organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="8"
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clone_lib="RPCI-24"
791. .1839
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20684. .20799
/rpt_family="MalR"
22901. .22957
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/rpt_family="Alu"
24384. .24441
/rpt_family="B4"
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)539. .2068?
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rpt family="Alu"
8974. .19317
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9821. .20013
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973. .4026
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?2968. .23000
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rpt family="B2"
0188. .20538
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8347.3845
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846. .3972
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